



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105844

TO: Malgorzata Walicka
Location: cm1/10d06/10d01
Art Unit: 1652
Wednesday, October 15, 2003

Case Serial Number: 10/054295

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Walicka,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



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Result No.	Score	Query Match	§			DB	ID	Description
			Length	DB	ID			
1	4015	100.0	4015	1	PCN-US03-19844-1	Sequence 1, Appli		
2	4015	100.0	4015	5	US-09-721-456-1	Sequence 1, Appli		
3	408.6	99.8	4037	5	US-09-721-456-343	Sequence 343, App		
4	3849.2	95.9	4029	5	US-09-721-456-292	Sequence 292, App		
5	364.1	97.9	3855	5	US-09-721-456-4	Sequence 4, Appli		
6	2205.2	54.9	3451	5	US-09-721-456-721	Sequence 721, App		
7	2200.8	54.8	3396	5	US-09-721-456-639	Sequence 639, App		
8	2196.6	54.7	3396	5	US-09-721-456-638	Sequence 638, App		
9	1860.4	48.8	2176	5	US-09-721-456-3	Sequence 3, Appli		
10	1877.2	46.8	2171	5	US-09-721-456-266	Sequence 266, App		
11	1862.2	46.4	3396	5	US-09-721-456-642	Sequence 642, App		
12	1756	43.7	3396	5	US-09-721-456-641	Sequence 641, App		
13	1670.6	41.6	4170	1	PCN-US03-19844-5	Sequence 5, Appli		
14	1600.8	39.9	3426	1	PCN-US03-19844-3	Sequence 3, Appli		
15	1542.2	38.4	3396	5	US-09-721-456-640	Sequence 640, App		
16	1515.8	37.8	4335	5	US-09-721-456-6	Sequence 6, Appli		
17	1515.8	37.8	15418	6	US-10-674-836-1	Sequence 1, Appli		
18	967	24.1	1758	1	PCN-US03-19844-7	Sequence 7, Appli		
19	741.4	18.5	2231	1	PCN-US03-19844-9	Sequence 9, Appli		
20	471.2	11.7	7498	6	US-10-674-836-2	Sequence 2, Appli		
21	442.4	11.0	2855	1	PCN-US03-19844-11	Sequence 11, Appli		
22	385.8	9.6	389	5	US-09-721-456-8	Sequence 8, Appli		
23	182	4.5	182	5	US-09-721-456-9	Sequence 9, Appli		
24	97.6	2.4	240	5	US-09-721-456-7	Sequence 7, Appli		
25	67.6	1.7	90	5	US-09-721-456-697	Sequence 697, App		
26	67.6	1.7	9795	7	US-60-501-821-44	Sequence 44, Appli		

Db	301	 CCGAGTGTCTGACAGGCTGTGCGACGCGGGCGGAAGAACGTGTGGCTTCGGCTTCGC	360
Qy	361	 GCTGCTGGACGGGGCCGCGGGGGCCCCCGAGGCCCTTACCACACAGCGTGGCAGCTA	420
Db	361	 GCTGCTGGACGGGGCCGCGGGGGCCCCCGAGGCCCTTACCACACAGCGTGGCAGCTA	420
Qy	421	 CCTGCCCAACACGGTGACCGACAGCACTGCGGGGAGGGGGCGTGGGGCTGTCTGTGCG	480
Db	421	 CCTGCCCAACACGGTGACCGACAGCACTGCGGGGAGGGGGCGTGGGGCTGTCTGTGCG	480
Qy	481	 CCGCGTGGGGACACAGTGTCTGTTTACCTCTGCTGCGACGCTTGTGTGCTGGT	540
Db	481	 CCGCGTGGGGACACAGTGTCTGTTTACCTCTGCTGCGACGCTTGTGTGCTGGT	540
Qy	541	 GGCTCCACAGCTGCGCCTACCAGGTGTGGGGCGCGCGCTGTACCAGCTTCGGCGGTGCCAC	600
Db	541	 GGCTCCACAGCTGCGCCTACCAGGTGTGGGGCGCGCGCTGTACCAGCTTCGGCGGTGCCAC	600
Qy	601	 TCAGGCGCGGCCCGCCGACACAGCTAGTGGACCCGGAAGGCGTCTGGGATGCGAACGGCG	660
Db	601	 TCAGGCGCGGCCCGCCGACACAGCTAGTGGACCCGGAAGGCGTCTGGGATGCGAACGGCG	660
Qy	661	 CTGGAACCATAGCTGACGGAGGCGGGGTCCCTTGGGCTGCCAGCCCGGGTGGCG	720
Db	661	 CTGGAACCATAGCTGACGGAGGCGGGGTCCCTTGGGCTGCCAGCCCGGGTGGCG	720
Qy	721	 GAGCGCGGGGGCAGTGCCACGCCGAAGTCTGTCCCTTGCCCAAGAGGCCAGGCGTGGCGC	780
Db	721	 GAGCGCGGGGGCAGTGCCACGCCGAAGTCTGTCCCTTGCCCAAGAGGCCAGGCGTGGCGC	780
Qy	781	 TGCCCCGTAGCGGAGCGGAGCGCCGTTGGGACGGGTTCCTTGGGCCACCCGGCAGGAC	840
Db	781	 TGCCCCGTAGCGGAGCGGAGCGCCGTTGGGACGGGTTCCTTGGGCCACCCGGCAGGAC	840
Qy	841	 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTTGTCTGCTGAGAGCCCGCGGAAGC	900
Db	841	 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTTGTCTGCTGAGAGCCCGCGGAAGC	900
Qy	901	 CACCTCTTTTGGAGGTCGCTCTCTGACGCGGCCACTTCCACCCATCCCTGGGCGCGCA	960
Db	901	 CACCTCTTTTGGAGGTCGCTCTCTGACGCGGCCACTTCCACCCATCCCTGGGCGCGCA	960
Qy	961	 GCACCAGCGGGCCCCCCTTCCACATCGGGGCCACACGTCCTCTGGGACAGCCTTGTCC	1020
Db	961	 GCACCAGCGGGCCCCCCTTCCACATCGGGGCCACACGTCCTCTGGGACAGCCTTGTCC	1020
Qy	1021	 CCGGTGTACGCGAGACCAAGCACTTCTTACTCTCTCAGGCGCACAGGACAGCTGGC	1080
Db	1021	 CCGGTGTACGCGAGACCAAGCACTTCTTACTCTCTCAGGCGCACAGGACAGCTGGC	1080
Qy	1081	 GCCTCTCTTCTACTCAGCTCTCTGAGGCCACAGCTGACTGGGCTCGGAGGCTGTGGGA	1140
Db	1081	 GCCTCTCTTCTACTCAGCTCTCTGAGGCCACAGCTGACTGGGCTCGGAGGCTGTGGGA	1140
Qy	1141	 GACCATCTTTCCTGGGTTCCAGGCCCTTGATGTCAGGAGTCCCGCAGGTTGCCCGGCT	1200
Db	1141	 GACCATCTTTCCTGGGTTCCAGGCCCTTGATGTCAGGAGTCCCGCAGGTTGCCCGGCT	1200
Qy	1201	 GCCCCAGCGTACTTGGCAAAATGGGGCCCCCTGTGTTCTGAGCTGTGGGAACCAACGCGCA	1260
Db	1201	 GCCCCAGCGTACTTGGCAAAATGGGGCCCCCTGTGTTCTGAGCTGTGGGAACCAACGCGCA	1260
Qy	1261	 GTGCCCTTACGGGTGCTCTCAAGAGGCACTGCCGCTCGGAGCTGGGTACCCCGCAGC	1320
Db	1261	 GTGCCCTTACGGGTGCTCTCAAGAGGCACTGCCGCTCGGAGCTGGGTACCCCGCAGC	1320
Qy	1321	 AGCCGCTGTCTGTGCCCGGAGAACCCACAGGCTCTGTGGCGGCCCGCCAGGAGGAGA	1380
Db	1321	 AGCCGCTGTCTGTGCCCGGAGAACCCACAGGCTCTGTGGCGGCCCGCCAGGAGGAGA	1380
Qy	1381	 CACAGACCCCGTGGTGTGACGTGTCTCCGCGACACAGCAGCCCCCTGGCAGGTGTA	1440

Db	1381	CACAGACCCCGCTGCCTGGTGCAGCTGCTCCGCCACGACAGCAGCGCCCTGCGAGGTGA	1440
QY	1441	CGGCTTCGTGGGGCCCTGCCTGGCGCGCTGGTGGCCCCAGAGCCTCTGGGGCTCAGGCA	1500
Db	1441	CGGCTTCGTGGGGCCCTGCCTGGCGCGCTGGTGGCCCCAGAGCCTCTGGGGCTCAGGCA	1500
QY	1501	CAACGAACCGCGCTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAAGCATGCCAA	1560
Db	1501	CAACGAACCGCGCTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAAGCATGCCAA	1560
QY	1561	GCTCTCGTCGAGAGCTGACGTGGGAAGATGAGCGTGGGGACTGCGCTTGGCTGGCGAG	1620
Db	1561	GCTCTCGTCGAGAGCTGACGTGGGAAGATGAGCGTGGGGACTGCGCTTGGCTGGCGAG	1620
QY	1621	GAGCCAGGGTTCGGCTGCTTCGGCGCCGAGACCGCTCTGCTGCTGAGAGATCCTGGC	1680
Db	1621	GAGCCAGGGTTCGGCTGCTTCGGCGCCGAGACCGCTCTGCTGCTGAGAGATCCTGGC	1680
QY	1681	CAAGTTCCTGCACTGGCTGATGATGTGTACGTCTCGAGCTGCTCAGCTCTTCTTTT	1740
Db	1681	CAAGTTCCTGCACTGGCTGATGATGTGTACGTCTCGAGCTGCTCAGCTCTTCTTTT	1740
QY	1741	TGTCAGGAGACACAGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
Db	1741	TGTCAGGAGACACAGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1801	CAAGTTCGAAGCATTGGATCATCAGACGACTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
Db	1801	CAAGTTCGAAGCATTGGATCATCAGACGACTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
QY	1861	GGAAGCAGAGCTCAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCG	1920
Db	1861	GGAAGCAGAGCTCAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCG	1920
QY	1921	CTTCATCCCAAGCCTCAGCGGCTGCGGCGGATGTGTGAACATGGACTACGTCGTTGGAGC	1980
Db	1921	CTTCATCCCAAGCCTCAGCGGCTGCGGCGGATGTGTGAACATGGACTACGTCGTTGGAGC	1980
QY	1981	CAGAACCTTCGGCAGAGAAAGAGCGCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACCTTCGGCAGAGAAAGAGCGCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTCTCAACTACGAGGGCGCGGCGCCCGGCTCTCTGGCGCTCTGTGCTGGG	2100
Db	2041	CAGCGTCTCAACTACGAGGGCGCGGCGCCCGGCTCTCTGGCGCTCTGTGCTGGG	2100
QY	2101	CCTGGACGATATCCACAGGGCCTGGGCGACACTTCGTGCTGCTGTCGGGGCCAGGACCC	2160
Db	2101	CCTGGACGATATCCACAGGGCCTGGGCGACACTTCGTGCTGCTGTCGGGGCCAGGACCC	2160
QY	2161	GCSCCTGAGCTCTACTTTGTCAAGTGTGATGTGACGGGGCGGTACGACACCATCCCCCA	2220
Db	2161	GCSCCTGAGCTCTACTTTGTCAAGTGTGATGTGACGGGGCGGTACGACACCATCCCCCA	2220
QY	2221	GGACAGGCTCACGGAGTCTATCGCCAGCATCATCAAAACCCAGAACAGTACTGGCTGG	2280
Db	2221	GGACAGGCTCACGGAGTCTATCGCCAGCATCATCAAAACCCAGAACAGTACTGGCTGG	2280
QY	2281	TCGGTATGCGGTTCAGAGGCCCGCCATGGCACGTCCGCAAGGCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCGGTTCAGAGGCCCGCCATGGCACGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2341	CGTCTCTACCTTGACAGACCTCAGCGCGTACATGGGACAGTTTCGTGGCTCACTGTCAGGA	2400
Db	2341	CGTCTCTACCTTGACAGACCTCAGCGCGTACATGGGACAGTTTCGTGGCTCACTGTCAGGA	2400
QY	2401	GACCAGCCGCTCAGAGGATGCGGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
Db	2401	GACCAGCCGCTCAGAGGATGCGGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2461	CAGTGGCCTTTCGACGCTCTCTTACGCTTTCATGTGCCACACGCGCTGCGCATCAGGG	2520
Db	2461	CAGTGGCCTTTCGACGCTCTCTTACGCTTTCATGTGCCACACGCGCTGCGCATCAGGG	2520

Qy	2521	CAAGTCTCTACGTCAGTGCAGGGAATCCCGCAGGGGTCCATCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTCTACGTCAGTGCAGGGAATCCCGCAGGGGTCCATCTCTCCACGCTGCTCTG	2580
Qy	2581	CAGCCTCTGCTACGGCAGCATGGAGAACAGCTGTTTTCGGGGATTCGGGGGACGGGCT	2640
Db	2581	CAGCCTCTGCTACGGCAGCATGGAGAACAGCTGTTTTCGGGGATTCGGGGGACGGGCT	2640
Qy	2641	GCTCCTCGGTTTGGTGGATGATTCTTGTGTGGTGACACCTCACCTCACCCACCGGAAAC	2700
Db	2641	GCTCCTCGGTTTGGTGGATGATTCTTGTGTGGTGACACCTCACCTCACCCACCGGAAAC	2700
Qy	2701	CTTCTCTCAGGACCTTGTCGAGGTGTCCTGAGTAGTGCGTGGTGAACATTGCGGAA	2760
Db	2701	CTTCTCTCAGGACCTTGTCGAGGTGTCCTGAGTAGTGCGTGGTGAACATTGCGGAA	2760
Qy	2761	GACAGTGGTGAACCTTCCCTCTAGAACGAGGCGCTGGGTGGCAGCGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGGTGAACCTTCCCTCTAGAACGAGGCGCTGGGTGGCAGCGCTTTTGTTCAGAT	2820
Qy	2821	GCGGGCCACGGGCTATTCCCTCTGGTGGCGGCTGCTGCTGATACCGGACCGCTGAGGT	2880
Db	2821	GCGGGCCACGGGCTATTCCCTCTGGTGGCGGCTGCTGCTGATACCGGACCGCTGAGGT	2880
Qy	2881	GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Db	2881	GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Qy	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCCGAACCTTTTGGGGTCTTGGGGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCCGAACCTTTTGGGGTCTTGGGGCTGAAGTG	3000
Qy	3001	TCACAGCCTGTCTTCTGGATTTCGAGGTGAACAGCTCCACAGCGGTGTGACCAACATCTA	3060
Db	3001	TCACAGCCTGTCTTCTGGATTTCGAGGTGAACAGCTCCACAGCGGTGTGACCAACATCTA	3060
Qy	3061	CAAGATCCTCTGCTGCAGGCGTACAGGTTTCACGATGTGCTCGAGCTCCCATTTTCA	3120
Db	3061	CAAGATCCTCTGCTGCAGGCGTACAGGTTTCACGATGTGCTCGAGCTCCCATTTTCA	3120
Qy	3121	TCAGCAAGTTTGGAAAGACCCACATTTTTCCTGGGGTCTATCTCTGACAGGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAAAGACCCACATTTTTCCTGGGGTCTATCTCTGACAGGCTCCCT	3180
Qy	3181	CTGCTACTCTCATCTGAAAGCCAAAGAACGAGGATGTGCTGGGGCCAAAGGCGCCG	3240
Db	3181	CTGCTACTCTCATCTGAAAGCCAAAGAACGAGGATGTGCTGGGGCCAAAGGCGCCG	3240
Qy	3241	CGGCCCCCTGCCCTCGAGGCGGTGACAGTGGCTGTGCCAACAGCATTCCTGCTCAAGCT	3300
Db	3241	CGGCCCCCTGCCCTCGAGGCGGTGACAGTGGCTGTGCCAACAGCATTCCTGCTCAAGCT	3300
Qy	3301	GACTCGACACCGGTGTACACTTACGTGCCACTTCTGGGGTCACTCAGGACGCCAGACGA	3360
Db	3301	GACTCGACACCGGTGTACACTTACGTGCCACTTCTGGGGTCACTCAGGACGCCAGACGA	3360
Qy	3361	GCTGAGTTCGGAAGTCTCCGGGGAGAGCGTACTGCCCTGAGGCGCCAGCAACCGGC	3420
Db	3361	GCTGAGTTCGGAAGTCTCCGGGGAGAGCGTACTGCCCTGAGGCGCCAGCAACCGGC	3420
Qy	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCGCCCCACAGCGCCGA	3480
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCGCCCCACAGCGCCGA	3480
Qy	3481	GAGCAGACACGAGCCCTGTACGCCGGGCTTACGTCCAGGAGGAGGGGGCGGC	3540
Db	3481	GAGCAGACACGAGCCCTGTACGCCGGGCTTACGTCCAGGAGGAGGGGGCGGC	3540
Qy	3541	CACACCCAGCCGACCGCTGGAGTCTGAGGCCTGAGTGTGTTGGCCAGGCGCTG	3600
Db	3541	CACACCCAGCCGACCGCTGGAGTCTGAGGCCTGAGTGTGTTGGCCAGGCGCTG	3600

RESULT 2
US-09-721-456-1
; Sequence 1, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-Nov-2000
; CLASSIFICATION: [Unknown]
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997

Db	1621	GAGCCAGGGTTGGCTGTGTTCCGGCCGACAGACCGCTCTGCGTGAGGAGATCCTGGC	1680
Qy	1681	CAAGTTCCTGCATGGCTGATGAGTGTGACGTGCTCGAGTGCTCAAGTCTTCTTTTA	1740
Db	1681	CAAGTTCCTGCATGGCTGATGAGTGTGACGTGCTCGAGTGCTCAAGTCTTCTTTTA	1740
Qy	1741	TGTCACGGAGACCACTTTTCAAAAGAACAGCTCTTTTTCACCGGAAGAGTGCTCGAG	1800
Db	1741	TGTCACGGAGACCACTTTTCAAAAGAACAGCTCTTTTTCACCGGAAGAGTGCTCGAG	1800
Qy	1801	CAAGTTCGAAAGCATGGAATCAGACAGCACTTGAAGAGGTCAGCTGCGGGAGCTGTC	1860
Db	1801	CAAGTTCGAAAGCATGGAATCAGACAGCACTTGAAGAGGTCAGCTGCGGGAGCTGTC	1860
Qy	1861	GGAGCAGAGTCCAGGAGCATCGGGAAGCAGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Db	1861	GGAGCAGAGTCCAGGAGCATCGGGAAGCAGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Qy	1921	CTTCATCCCAAGCCTCAGCGGCTGCGGCCGATTTGAAACATGGACTACGTCGTGGGAGC	1980
Db	1921	CTTCATCCCAAGCCTCAGCGGCTGCGGCCGATTTGAAACATGGACTACGTCGTGGGAGC	1980
Qy	1981	CAGAACCTTCGCGAGAAAGAGGCGCGAGCGCTCCACCTCGAGGCTGAAGGCACCTGTT	2040
Db	1981	CAGAACCTTCGCGAGAAAGAGGCGCGAGCGCTCCACCTCGAGGCTGAAGGCACCTGTT	2040
Qy	2041	CAGCGTCTCAACTACAGCGGGCGGGCCCGCCCGGCTCTGCGGCCCTCTGTGCTGGG	2100
Db	2041	CAGCGTCTCAACTACAGCGGGCGGGCCCGCCCGGCTCTGTGCTGGG	2100
Qy	2101	CCTGGAGCATATCACAGGCGCTGGCGACCTTCGTGCTGCTGCGGGCCCGCAGGACCC	2160
Db	2101	CCTGGAGCATATCACAGGCGCTGGCGACCTTCGTGCTGCTGCGGGCCCGCAGGACCC	2160
Qy	2161	GCGCGCTGAGCTGTACTTTGCAAGTGGATGTGACGGGCGCTACGACACCATCCCCCA	2220
Db	2161	GCGCGCTGAGCTGTACTTTGCAAGTGGATGTGACGGGCGCTACGACACCATCCCCCA	2220
Qy	2221	GGACAGCTCAGGAGTGCATGCCAGCATCATCAAAACCCAGAACAGTACTGCTGGG	2280
Db	2221	GGACAGCTCAGGAGTGCATGCCAGCATCATCAAAACCCAGAACAGTACTGCTGGG	2280
Qy	2281	TCGCTATGCCGTGTCAGAAAGCGCGCCATGGCAGCTCCGCAAGCCCTTCAAGAGCCA	2340
Db	2281	TCGCTATGCCGTGTCAGAAAGCGCGCCATGGCAGCTCCGCAAGCCCTTCAAGAGCCA	2340
Qy	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
Qy	2401	GACGAGCCGCTGAGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
Db	2401	GACGAGCCGCTGAGGATGCCGTGTCATCGAGCAGAGTCCCTCCCTGAATGAGGCCAG	2460
Qy	2461	CAGTGGCCTCTTGACGCTCTTCTACGCTTTCATGTGCCACACCGCTGCGCATCAGGG	2520
Db	2461	CAGTGGCCTCTTGACGCTCTTCTACGCTTTCATGTGCCACACCGCTGCGCATCAGGG	2520
Qy	2521	CAAGTCTTACGTCAGTGCAGGGGATCCGCGAGGGTCCATCCTCTCCAGCTGCTCTG	2580
Db	2521	CAAGTCTTACGTCAGTGCAGGGGATCCGCGAGGGTCCATCCTCTCCAGCTGCTCTG	2580
Qy	2581	CAGCCTGTGTACGGCAGCATGGAGAACAGCTGTTTGGGGGATTCGGGGGACGGGCT	2640
Db	2581	CAGCCTGTGTACGGCAGCATGGAGAACAGCTGTTTGGGGGATTCGGGGGACGGGCT	2640
Qy	2641	GCTCCTCGCTTGGTGATGATTTCTTGGTGACACCTCACCTCACCCACGCGAAGAAC	2700
Db	2641	GCTCCTCGCTTGGTGATGATTTCTTGGTGACACCTCACCTCACCCACGCGAAGAAC	2700
Qy	2701	CTTCCTCAGGACCTGCTCGAGGTGTCCTGAGTATGGCTGCTGAGTATGGCTGCTGCGGAA	2760
Db	2701	CTTCCTCAGGACCTGCTCGAGGTGTCCTGAGTATGGCTGCTGAGTATGGCTGCTGCGGAA	2760
Qy	2761	GACAGTGGTAACATTCCTCTGTAGAAAGACGAGGCGCTTGGGTGGCACGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGGTAACATTCCTCTGTAGAAAGACGAGGCGCTTGGGTGGCACGGCTTTTGTTCAGAT	2820
Qy	2821	GCGGGCCACGGCTATTTCCCTGCTGGTGGCGCTCTGCTGGATACCCGGACCCCTGGAGGT	2880
Db	2821	GCGGGCCACGGCTATTTCCCTGCTGGTGGCGCTCTGCTGGATACCCGGACCCCTGGAGGT	2880
Qy	2881	GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTTCAACCG	2940
Db	2881	GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTTCAACCG	2940
Qy	2941	CGGCTTCAAGGCTGGGAGAACATCGCTCGGAAACTCTTTGGGGTCTTTGGGGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGAACATCGCTCGGAAACTCTTTGGGGTCTTTGGGGCTGAAGTG	3000
Qy	3001	TCACAGCTGCTTTCTGGATTTGCAAGTGAACAGCTCCAGACGCTGTCACACCAACATCTA	3060
Db	3001	TCACAGCTGCTTTCTGGATTTGCAAGTGAACAGCTCCAGACGCTGTCACACCAACATCTA	3060
Qy	3061	CAAGATCCTCTGCTCAGGCGTACAGGTTTTCAGCATGTGCTGCGAGCTCCCATTTTCA	3120
Db	3061	CAAGATCCTCTGCTCAGGCGTACAGGTTTTCAGCATGTGCTGCGAGCTCCCATTTTCA	3120
Qy	3121	TCAGCAAGTTTGGAAACCCCAATTTTCTCGCGCTCATCTCTGACAGGGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAAACCCCAATTTTCTCGCGCTCATCTCTGACAGGGCTCCCT	3180
Qy	3181	CTGCTACTCATCTGAAAGCCCAAGACGAGGATGTGCTGCGGGCCCAAGGCGCGCG	3240
Db	3181	CTGCTACTCATCTGAAAGCCCAAGACGAGGATGTGCTGCGGGCCCAAGGCGCGCG	3240
Qy	3241	CGGCGCTCTGCGCTCCGAGGCGCTGACGTGCTGCCACCAAGCATTCCTGCTCAAGCT	3300
Db	3241	CGGCGCTCTGCGCTCCGAGGCGCTGACGTGCTGCCACCAAGCATTCCTGCTCAAGCT	3300
Qy	3301	GACTCGACACGGTGTCACTTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGCGCA	3360
Db	3301	GACTCGACACGGTGTCACTTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGCGCA	3360
Qy	3361	GCTGAGTGGGAAGCTCCCGGGGACGCTGACTGCGCTGGAGCGCAGCCCAACCGGC	3420
Db	3361	GCTGAGTGGGAAGCTCCCGGGGACGCTGACTGCGCTGGAGCGCAGCCCAACCGGC	3420
Qy	3421	ACTGCCCTCAGACTTCAAGACCATCTTGACTGTATGGCCACCCGCCACAGCCAGCGCA	3480
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTTGACTGTATGGCCACCCGCCACAGCCAGCGCA	3480
Qy	3481	GAGCAGACACGAGCCCTGTACGGCGGCTCTACGTCCCAAGGAGGAGGGCGGCGC	3540
Db	3481	GAGCAGACACGAGCCCTGTACGGCGGCTCTACGTCCCAAGGAGGAGGGCGGCGC	3540
Qy	3541	CACACCAAGCCCGCCAGCGCTGGGAGTCTGAGGCGCTGAGTCAAGTGTGGCCGAGGCGCTG	3600
Db	3541	CACACCAAGCCCGCCAGCGCTGGGAGTCTGAGGCGCTGAGTCAAGTGTGGCCGAGGCGCTG	3600
Qy	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGCTGAGGCGCTGAGGAGTGTCCAGCCAAAGGCT	3660
Db	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGCTGAGGCGCTGAGGAGTGTCCAGCCAAAGGCT	3660
Qy	3661	GAGTGTCCAGCACACCTTGCCTCTTCACTTCCCAAGGCTGGGCTCGGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGCACACCTTGCCTCTTCACTTCCCAAGGCTGGGCTCGGCTCCACCCCA	3720
Qy	3721	GGGCGAGCTTTCTCACCAGGAGCGCGCTTCCACTCCCGCATAGATAGTCCATCC	3780
Db	3721	GGGCGAGCTTTCTCACCAGGAGCGCGCTTCCACTCCCGCATAGATAGTCCATCC	3780
Qy	3781	CCAGATTGCGCATTGTTTCAACCCCTCGCCTCTCTTTGCTTTCACCCACCACTCC	3840
Db	3781	CCAGATTGCGCATTGTTTCAACCCCTCGCCTCTCTTTGCTTTCACCCACCACTCC	3840

Qy	1	GCAGCGTGGGTCTTCTGTCGCACTGCGAAGCCCTTGGCCCCCGGCACACCCCGCATGCC	60
Db	1	GCAGCGTGGGTCTTCTGTCGCACTGCGAAGCCCTTGGCCCCCGGCACACCCCGCATGCC	60
Qy	61	GCAGCGTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	120
Db	61	GCAGCGTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	120
Qy	121	CGCGCTGGCCACCTTCTGTGGCGCCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGG	180
Db	121	CGCGCTGGCCACCTTCTGTGGCGCCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGG	180
Qy	181	GGACCCGGCGGCTTTCCGGCGCTGTGTGGCCCCCAGTGCCTGGTGTGGTGCCTTGGAGCG	240
Db	181	GGACCCGGCGGCTTTCCGGCGTGTGTGGCCCCANTGCTGGTGTGGTGCCTTGGGANGN	240
Qy	241	ACGGCGCCCCCGCGCCCCCTTCTTCCGCCAGGTGTCTTGCCTGAAGAGCTGGTGGC	300
Db	241	ANGCGNCCCCCGCGCCCCCTTCTTCCGCCAGGTGTCTTGCCTGAANGANTGGTGGC	300
Qy	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGGAAGACTGCTGGCTTCGGCTTCGC	360
Db	301	CCGAGTCTGCANANGCTGTGCGANGCGCGCGGAANAACGTGCTGGCTTCGGCTTCGC	360
Qy	361	GCTGCTGGACGGGGCCCCGGGGCCCCCCCCAGGGCTTCAACACAGCGTGCAGCTA	420
Db	361	GCTGCTGGACGGGGCCCCGGGGCCCCCCCCAGGGCTTCAACACAGCGTGCAGCTA	420
Qy	421	CCTGCCCAACAGGCTGACCGACCGACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGG	480
Db	421	CCTGCCCAACAGGCTGACCGACCGACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGG	480
Qy	481	CCGCGTGGGGAGACGTGCTGGTTCACTGCTTGGCACGCTGCGCGCTCTTTGTGTGCTGT	540
Db	481	CCGCGTGGGGAGACGTGCTGGTTCACTGCTTGGCACGCTGCGCGCTTTTGTGTGCTGT	540
Qy	541	GGCTCCAGCTGGCCCTACAGGTGTGCGGGCGCGCGCTGTACTACGCTGGGCGTGCAC	600
Db	541	GGNTCCAGCTGGCCCTACCANGTGTGCGGGCGCGCGCTGTACTACGCTGGGCGTGCNAC	600
Qy	601	TCAGGCGCGCCCCCGCCACACGCTAGTGACCCCGAAGCGCTCGGATGCGAAGCGGCG	660
Db	601	TCAGGCGCGCCCCCGCCACACGCTAGTGACCCCGAAGCGCTCGGATGCGAAGCGGCG	660
Qy	661	CTGGAACCATAGCGTCAAGGAGCGCGGGTTCCTTGGCGCTGCCAGCCCGGGTGCAG	720
Db	659	CTGGAACCATAGCGTCAAGGAGCGCGGGTTCCTTGGCGCTGCCAGCCCGGGTGCAG	717
Qy	721	GAGCGCGGGGCGAGTGCACAGCAAGTGTGCGTTGCCCCAAGAGGCGCAGCGTGGCG	780
Db	718	GAGCGCGGGGCGAGTGCACAGCAAGTGTGCGTTGCCCCAAGAGGCGCAGCGTGGCG	777
Qy	781	TGCCCTTGACCGAGCGGAGCGCGTTGGGAGGGGTCTTGGGCCACCCCGGCGAGGAC	840
Db	778	TGCCCTTGAGCGGAGCGGAGCGCGTTGGGAGGGGTCTTGGGCCACCCCGGCGAGGAC	837
Qy	841	CGGTGGACCGAGTGACCGTGTGTTTCTGTGTGGTGTCACTTGCACAGCCCGCCGAAAGC	900
Db	838	GCCTGGACCGAGTGACCGTGTGTTTCTGTGTGGTGTCACTTGCACAGCCCGCCGAAAGC	897
Qy	901	CACCTCTTTGGAGGGTGGGTCTCTGTGCAAGCGGCACTCCCAACCAATCGGTGGGCGCCA	960
Db	898	CACCTCTTTGGAGGGTGGGTCTCTGTGCAAGCGGCACTCCCAACCAATCGGTGGGCGCCA	957
Qy	961	GCACCGCGGGCCCCCATCCACATCGCGGCGACACGTCCTTGGGACACGCTTGTTC	1020
Db	958	GCACCGCGGGCCCCCATCCACATCGCGGCGACACGTCCTTGGGACACGCTTGTTC	1016
Qy	1021	CCCGGTGTACCGCGAGACCAAGCACTTCTTCTACTCTCAGGGCGACAAGGACGAGTGGC	1080
Db	1017	CCCGGTGTACCGCGAGACCAAGCACTTCTTCTACTCTCAGGGCGACAAGNA--CACTGGC	1074
Qy	1081	GCCCTCTCTTCTACTC-AGCTCTCTGAGGCCCCAGCCTTACTTGGCGCTCGGAGGCTCGTGG	1139

[illegible]

Db 2154 CGCGCGCTGAGCTGACTTTGTCAGAGTGGATGTACGGGCGCTACGACACCATCCCC 2213
QY 2219 CAGGACAGCTCAGCGAGGTGATCGCCAGCATCATCAAAACCCAGAACACGCTACTGCGTG 2278
Db 2214 CAGGACAGCTCAGCGAGGTGATCGCCAGCATCATCAAAACCCAGAACACGCTACTGCGTG 2273
QY 2279 GTCGGTATGCGTGGTCCAGAGGCCCGCCATGGGACGCTCCGCAAGSCCTTCAAGAGC 2338
Db 2274 GTCGGTATGCGTGGTCCAGAGGCCCGCCATGGGACGCTCCGCAAGSCCTTCAAGAGC 2333
QY 2339 CACGCTCTACTCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTCGCTCAGCTGCG 2398
Db 2334 CACGCTCTACTCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTCGCTCAGCTGCG 2393
QY 2399 GAGACAGCCGCTGAGGATGCGCTGTCATCGAGAGAGCTCTCTCCCTGAATGAGGCC 2458
Db 2394 GANAACAGCCGCTGAGGATGCGCTGTCATCGAGAGAGCTCTCTCCCTGAATGAGGCC 2453
QY 2459 AGCAGTGGCCTTTCGAGCGTCTTCTACGCTTTCATGTGCCACGCGCTGCGCATCAGG 2518
Db 2454 AGCAGTGGCCTTTCGAGCGTCTTCTACGCTTTCATGTGCCACGCGCTGCGCATCAGG 2513
QY 2519 GGCAGTCTACTGTCAGTCCAGCGGATCCCGAGGATCCCGAGGCTCCATCTCTCCAGCTGCTC 2578
Db 2514 GGCAGTCTACTGTCAGTCCAGCGGATCCCGAGGATCCCGAGGCTCCATCTCTCCAGCTGCTC 2573
QY 2579 TGCAGCCTGCTCAGCGGACATGGAGAACAGCTGTTTGGGGATTCGCGGGAGCGG 2638
Db 2574 TGCAGCCTGCTCAGCGGACATGGAGAACAGCTGTTTGGGGATTCGCGGGAGCGG 2633
QY 2639 CTGCTCTCCGCTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAA 2698
Db 2634 CTGCTCTCCGCTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAA 2693
QY 2699 ACCTTCTCAGAACCTGGTCCGAGGTGCTCCTGAGTATGCTGCGTGGTGAACCTTGCGG 2758
Db 2694 ACCTTCTCAGAACCTGGTCCGAGGTGCTCCTGAGTATGCTGCGTGGTGAACCTTGCGG 2753
QY 2759 AAGCAGTGGTGAACCTTCCCTGTAGAACAGAGGCCCTGGGTGGACGCGCTTTGTTTCAG 2818
Db 2754 AAGCAGTGGTGAACCTTCCCTGTAGAACAGAGGCCCTGGGTGGACGCGCTTTGTTTCAG 2813
QY 2819 ATCGCGGCCACGCGCTATTCCTCTGTCGCGCTGCTGCTGATACCCGACCCCTGGAG 2878
Db 2814 ATCGCGGCCACGCGCTATTCCTCTGTCGCGCTGCTGCTGATACCCGACCCCTGGAG 2873
QY 2879 GTGCAGAGCGACTACTCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAAC 2938
Db 2874 GTGCAGAGCGACTACTCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAAC 2933
QY 2939 CGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGTCTTCCGGCTGAAG 2998
Db 2934 CGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGTCTTCCGGCTGAAG 2993
QY 2999 TGTACAGCCCTGTTCTTGATTTGTCAGGTGAACAGCCCTCCAGAGCGGTGTCACCAACATC 3058
Db 2994 TGTACAGCCCTGTTCTTGATTTGTCAGGTGAACAGCCCTCCAGAGCGGTGTCACCAACATC 3053
QY 3059 TACAAGATPCTCTCTGTCAGSCGTACAGGTTTTCACGCATGTGTGCTCAGCTCCCATTT 3118
Db 3054 TACAAGATPCTCTCTGTCAGSCGTACAGGTTTTCACGCATGTGTGCTCAGCTCCCATTT 3113
QY 3119 CATCAGAGTTTGAAGAACCCACATTTTTCTGCGGCTCATCTCTGACACGCGCTCC 3178
Db 3114 CATCAGAGTTTGAAGAACCCACATTTTTCTGCGGCTCATCTCTGACACGCGCTCC 3173
QY 3179 CTCGTCTCTCATCTGTAAGCCAGAACCCAGGATGTGCTGGGGGCCAAGGGGCC 3238
Db 3174 CTCGTCTCTCATCTGTAAGCCAGAACCCAGGATGTGCTGGGGGCCAAGGGGCC 3233
QY 3239 GCCGGCCCTCTGCGCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGATTTCTGCTCAAG 3298
Db 3234 GCCGGCCCTCTGCGCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGATTTCTGCTCAAG 3293

QY 3299 CTGACTCGACACCGTGTCACTTACCTTACCTGACCTTCCCTGGGTCACTCAGGACACCCAGAGC 3358
Db 3294 CTGACTCGACACCGTGTCACTTACCTTACCTTCCCTGGGTCACTCAGGACACCCAGAGC 3353
QY 3359 CAGCTGAGTCCGGAAGCTCCCGGGAGCGCTGACTGCTCCCTGGAGCCCGCAGCCAGCCG 3418
Db 3354 CAGCTGAGTCCGGAAGCTCCCGGGAGCGCTGACTGCTCCCTGGAGCCCGCAGCCAGCCG 3413
QY 3419 GCACCTGCCCTCAGACTTCAAGACCATCTTGGACTGATGGCCACCCCGCCACAGCCAGGCC 3478
Db 3414 GCACCTGCCCTCAGACTTCAAGACCATCTTGGACTGATGGCCACCCCGCCACAGCCAGGCC 3473
QY 3479 GAGAGCAGACACCGACGACGCTTCAAGCCGCTTACGTCGCCGCTTACGTCGCCAGGAGGCGG 3538
Db 3474 GAGAGCAGACACCGACGACGCTTCAAGCCGCTTACGTCGCCGCTTACGTCGCCAGGAGGCGG 3533
QY 3539 CCCACACCCAGCCCGCAGCCGCTGGAGTCTGAGGCTGAGTGGTGGTGGTGGTGGTGGTGG 3598
Db 3534 CCCACACCCAGCCCGCAGCCGCTGGAGTCTGAGGCTGAGTGGTGGTGGTGGTGGTGGTGG 3593
QY 3599 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3658
Db 3594 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3653
QY 3659 CTGAGTGTCCAGACACCTGCGCTTCACTTCCCGACAGGCTGCGGCTCGGCTCCACCC 3718
Db 3654 CTGAGTGTCCAGACACCTGCGCTTCACTTCCCGACAGGCTGCGGCTCGGCTCCACCC 3713
QY 3719 CAGGCCAGCTTTTCTCACCAGGAGCCGCTTCCACTTCCCTCCCTCCCTCCCTCCCTCCCT 3778
Db 3714 CAGGCCAGCTTTTCTCACCAGGAGCCGCTTCCACTTCCCTCCCTCCCTCCCTCCCTCCCT 3773
QY 3779 CCCAGATTCGCTTTCACCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCT 3838
Db 3774 CCCAGATTCGCTTTCACCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCT 3833
QY 3839 CCAGTGTGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCT 3898
Db 3834 CCAGTGTGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCT 3893
QY 3899 TGCCCTGTACACGAGGAGGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCT 3958
Db 3894 TGCCCTGTACACGAGGAGGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCTTGAGAGACCT 3953
QY 3959 GGGAGTGTCTGGAGTAAATACTGAATATATGAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGT 4015
Db 3954 GGGAGTGTCTGGAGTAAATACTGAATATATGAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGT 4010

RESULT 5
US-09-721-456-4
; Sequence 4, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; ;
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Db	1261	GTCCCCCTACGGGGTCTCTCAAGACGCACTCCCGCTGCGAGCTGGGGTCAACCCAGC	1320
QY	1321	AGCCGGTGTCTGTGCGCGGAGAAAGCCCAAGGGCTCTGTGGCGGCCCGCCCGAGGAGGGA	1380
Db	1321	AGCCGGTGTCTGTGCGCGGAGAAAGCCCAAGGGCTCTGTGGCGGCCCGCCCGAGGAGGGA	1380
QY	1381	CACAGACCCCGTCCGCTGGTGTGAGCTGTCTCCGCCAGCACAGCAGCCCTGGCAGGTGA	1440
Db	1381	CACAGACCCCGTCCGCTGGTGTGAGCTGTCTCCGCCAGCACAGCAGCCCTGGCAGGTGA	1440
QY	1441	CGGCTTCTGTCGGGGCTGCTGCGCGGCTGGTGTGCGCCAGAGGCTCTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCTGTCGGGGCTGCTGCGCGGCTGGTGTGCGCCAGAGGCTCTGGGGCTCCAGGCA	1500
QY	1501	CAACGAACCGCGCTCTCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1560
Db	1501	CAACGAACCGCGCTCTCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1561	GCTCTGCTGCAGGAGCTGACGTGGAAGATGACGCTGCGGGACTGGCTGGCTGGCGCAG	1620
Db	1561	GCTCTGCTGCAGGAGCTGACGTGGAAGATGACGCTGCGGGACTGGCTGGCTGGCGCAG	1620
QY	1621	GAGCCAGGGTTGGCTGTCTCCGCCGAGAGCAGCGTCTGCGTGAGGAGATCTGGC	1680
Db	1621	GAGCCAGGGTTGGCTGTCTCCGCCGAGAGCAGCGTCTGCGTGAGGAGATCTGGC	1680
QY	1681	CAAGTTCTCTGCACTGATGATGTGTACGTCTGCGAGCTGCTCAGGCTCTTCTTTTA	1740
Db	1681	CAAGTTCTCTGCACTGATGATGTGTACGTCTGCGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1741	TGTCACGGAGACACCTTTCAAAGAACAGGCTCTTTTACCGGAAGAGTGTCTGGAG	1800
Db	1741	TGTCACGGAGACACCTTTCAAAGAACAGGCTCTTTTACCGGAAGAGTGTCTGGAG	1800
QY	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGGTGTCGCGGAGCTGTC	1860
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGGTGTCGCGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTGAGGAGCATCGGAAGCCAGGCGCGCCCTGCTGACGTCTCAGAGTCCG	1920
Db	1861	GGAAGCAGAGGTGAGGAGCATCGGAAGCCAGGCGCGCCCTGCTGACGTCTCAGAGTCCG	1920
QY	1921	CTTCATCCCAAGCTTGACGGGTGCGCGGATGTGAACATGACATGACATGACATGACAT	1980
Db	1921	CTTCATCCCAAGCTTGACGGGTGCGCGGATGTGAACATGACATGACATGACATGACAT	1980
QY	1981	CAGAACGTTCCGCGAGAGAAAGAGGCGCGAGCTCTCAGCTCAGGAGGTGAAGCACTGTT	2040
Db	1981	CAGAACGTTCCGCGAGAGAAAGAGGCGCGAGCTCTCAGCTCAGGAGGTGAAGCACTGTT	2040
QY	2041	CAGCGTGTCACTACAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2100
Db	2041	CAGCGTGTCACTACAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2100
QY	2101	CTGAGCAGATATCCAGAGGCTGCGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2160
Db	2101	CTGAGCAGATATCCAGAGGCTGCGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2160
QY	2161	GCGGCTGTGAGTCTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCACTCCCGCA	2220
Db	2161	GCGGCTGTGAGTCTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCACTCCCGCA	2220
QY	2221	GGACAGGCTCAGGAGGTGATCGCCAGAGTATCAAAACCCAGAACACGCTACTGCGTGGG	2280
Db	2221	GGACAGGCTCAGGAGGTGATCGCCAGAGTATCAAAACCCAGAACACGCTACTGCGTGGG	2280
QY	2281	TCGGTATGCGGTGCTCCAGAGCCCGCATGGCAGCTCCCGAAGSCCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCGGTGCTCCAGAGCCCGCATGGCAGCTCCCGAAGSCCTTCAAGAGCCA	2340
QY	2341	CGTCTCTACTTGTACAGACCTCCAGCGCTACATGCGACAGTTCTGCTGCTCAGCTGCGAG	2400
Db	2341	CGTCTCTACTTGTACAGACCTCCAGCGCTACATGCGACAGTTCTGCTGCTCAGCTGCGAG	2400
Db	2341	-----C-----	2341
QY	2401	GACCAGCCCGCTGAGGGATGCCGTGCTATGAGAGAGAGTCTCTCCTGAATGAGGCCAG	2460
Db	2342	-----	2341
QY	2461	CAGTGGCCCTCTTCGACGTCTCTCCTACGCTTCATGTGCCACACGCGCTGGCATCAGGGG	2520
Db	2342	-----	2341
QY	2521	CAAGTCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
Db	2342	---GTCTCTAGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCAGCTGCTCTG	2398
QY	2581	CAGCCTGTGCTACGGGACATGAGAACAAAGCTGTTTTCGGGGATTGGCGGACGCGGCT	2640
Db	2399	CAGCCTGTGCTACGGGACATGAGAACAAAGCTGTTTTCGGGGATTGGCGGACGCGGCT	2458
QY	2641	GCTCCTGCGTTGGTGGATGATTTCTTGTGTTGTTGACACCTCAGCTCACCACCGGGAAC	2700
Db	2459	GCTCCTGCGTTGGTGGATGATTTCTTGTGTTGTTGACACCTCAGCTCACCACCGGGAAC	2518
QY	2701	CTTCTCTCAGGACCTGCTCCGAGGTGTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2760
Db	2519	CTTCTCTCAGGACCTGCTCCGAGGTGTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2578
QY	2761	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGACGCGCTTTTGTTCAGAT	2820
Db	2579	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGACGCGCTTTTGTTCAGAT	2638
QY	2821	GCCGGCCACGCGCTATTTCCCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
Db	2639	GCCGGCCACGCGCTATTTCCCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2698
QY	2881	GCAGAGCGACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAGCTTCAACCG	2940
Db	2699	GCAGAGCGACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAGCTTCAACCG	2758
QY	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCCAAACTCTTTGGGCTCTTGGGCTGGAAGTG	3000
Db	2759	CGGCTTCAAGGCTGGGAGAACATGCGTCCAAACTCTTTGGGCTCTTGGGCTGGAAGTG	2818
QY	3001	TCACAGCTCTTCTGCTGATTTGAGGTGAACAGCTCCACAGCTGTCACACCAACATCTA	3060
Db	2819	TCACAGCTCTTCTGATTTGAGGTGAACAGCTCCACAGCTGTCACACCAACATCTA	2878
QY	3061	CAAGATCTCTCTGCTGACGCGTACAGGTTTACGCTATGCTGCTGCTGCTGCTGCTGCTG	3120
Db	2879	CAAGATCTCTCTGCTGACGCGTACAGGTTTACGCTATGCTGCTGCTGCTGCTGCTGCTG	2938
QY	3121	TCAGAGAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGACACGCGCTCCCT	3180
Db	2939	TCAGAGAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGACACGCGCTCCCT	2998
QY	3181	CTGCTACTCCATCTCTGAAAGCCAAAGACGAGGATGCTGCGGGCCGAGGCGCGCGC	3240
Db	2999	CTGCTACTCCATCTCTGAAAGCCAAAGACGAGGATGCTGCGGGCCGAGGCGCGCGC	3058
QY	3241	CGGCTCTGCTGCTGCGGCGCTGAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3300
Db	3059	CGGCTCTGCTGCTGCGGCGCTGAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3118
QY	3301	GACTCAGACCGTGTACCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3360
Db	3119	GACTCAGACCGTGTACCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3178
QY	3361	GCTGAGTCCGAAGCTCCCGGGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3420
Db	3179	GCTGAGTCCGAAGCTCCCGGGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3238
QY	3421	ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3480
Db	3239	ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3298

QY 476 CTGCGCGCGTGGCGAGCGAGCTGCTGTTCACTGCTGGACAGCTGGCGCTCTTTGTC 535
DB 448 CTGCGTGTGTGTGAGAGAGTCTGTGTTCACTGCTGGCTGCTGTGCTCTCTGTT 507
QY 536 CTGGTGGCTCCAGCTCGCGCTACAGGTGTGCGGGCGCGCGCTGTACAGCTCGGGCT 595
DB 508 CTGGTGTCTCGTCTCGCGCTTACAGGTGTGTGTTGCTCGCGCGCTGTACAGCTCGGGTCT 567
QY 596 GCGACTCAGGCGCGCGCGCGCGCGCGCTAGTGTGAGCCCGGAGAGCGCTGTGGATGCGAA 655
DB 568 GCTACCCAGAGTCTGCGCGCGCGCGCGCGCTTCCGCTCGCGCTCGTGTGGTGTGCGAA 627
QY 656 CGGCGCTGGAAACATAGCTCAGGAGCGCGGGTCCCGCTGGCGCTGCCAGCCCGGGT 715
DB 628 CGTGTGGAAACACTCGTTCGTGTAAGCTGTGTTCCGCTGGGTCTGCGGGCTCGGGGT 687
QY 716 GCGAGGAGCGCGGGGCACTGCGAGCGCGAAGTGTGCGCTGTGCGCAAGAGCGCCAGCGCT 775
DB 688 GCTCGTGTGTGTGTGCTCGCTTCCGCTTCCGCTGCGCGCTGCCGGAACGTTCCGCTGT 747
QY 776 GCGCTGCGCTGAGCGCGGAGCGAGCGCGCTGTGGGAGGAGGCTCTGGGCGCGCGGCG 835
DB 748 GGTGCTCTCCGGAACCGGAACGTTACCCCGGTGTGCTGAGGTTCTCGGGCTCACCCGGT 807
QY 836 AGGACGCTGTGACCGAGTGAACGCTGTCTGTGTGTGTACCTGCGACGACCGCGCGAA 895
DB 808 CGTACCGCTGTGCTCGTCCGACCGGTGTTCTGCTGTGTTTCCCGGCTGCTCGGGCTGAA 867
QY 896 GAAGCCACCTCTTTGAGGAGTGGCTCTGTGACGCGCGCACTCCCACTACCTCGTGGG 955
DB 868 GAAGTACCTTCCCTGGAAGTGTCTGTCCGGAACCGTCACTCCCACTCGTGGTGGT 927
QY 956 GCGCAGCACACGCGGCG 1015
DB 928 CGTACGACACACGCTGTGCTGCGCGCTCCACCTCGCGCGCGCGCGCGCGCGCGCG 987
QY 1016 TGTGCGCGCGGTACCGCGAGACCAAGCACTTCTCTACTTCTCCTCAGCGGACAGGAGCAG 1075
DB 988 TGCGCGCGGTGTACGCTGAAACCAACACTTCTGTACTCTCTCGGTGACAGAGAAC 1047
QY 1076 CTGGGCGCGCTCTCTCTACTCTAGCTCTCTGAGGCGCGAGCTGCTGCGCTCGGAGCTC 1135
DB 1048 CTGCGTCCGCT 1107
QY 1136 GTGAGACCATCTTCTGCGCTTCCAGCGCTGAGTGCAGGAGTCCCGCGAGTGTGCC 1195
DB 1108 GTTGAAACTATCT 1167
QY 1196 CGCTGCGCGCGCTACTTGGCAAAATCGCGCGCTGTTTCTGAGCTGCTTGGGAACAC 1255
DB 1168 GCTCTCGCGCAGCTTACTGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1227
QY 1256 GCGAGTGCCTCTACGGGCTGCTCTCTAAGACGACTGCGCGCTGCGAGCTGGGTCACC 1315
DB 1228 GCTCAGTGCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
QY 1316 CAGCAGCGCGTGTCTGCTGCGGAGAGCGCGCGAGGCTGTGTGGGCGCGCGCGAGGAG 1375
DB 1288 CCGGCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1347
QY 1376 GAGGACACAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1435
DB 1348 GAGATACGACCGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1407
QY 1436 GTGTAGGCTTCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1495
DB 1408 GTTTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1467
QY 1496 AGCAGACAGCGCGCTTCTCAGGACACCAAGATTCATCTCCCTGGGGAAGCAT 1555
DB 1468 CGTCACACAGAGCTGTCT 1527
QY 1556 GCCAAGCTCTCTGCGAGGAGCTGACGTGGAAGTGTGCTGCGGAGTGTGCGGCTGCTGCT 1615

DB 1528 GCTAAACTGTCCCTGCAAGAACTGACCTGGAAAAATGTCCGTTCGTGACTGCGCTTGGCTG 1587
QY 1616 CGCAGGAGCCAGGGGTGGCTGTTCGGCGCCGAGAGCACCGCTCTGCGTGGAGATC 1675
DB 1588 CGTGTCTCTCGGCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1647
QY 1676 CTGCGCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGCGAGCTGCTCAGGTCTTTC 1735
DB 1648 CTGCTAAATTCCTGCACTGGCTGATGTCGCTATACGTTGTGTAACCTGCTGCTGCTTCT 1707
QY 1736 TTTTATGTACGCGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTTCTACCGGAAGAGTCT 1795
DB 1708 TTTTACGTTTACCGAAACACCGTTTCCGAAAAACCGTCTGTTCTTCTTCTTCTTCTTCTT 1767
QY 1796 TGGAGCAAGTTCGAAGCATTTGAAATCAGACAGCACTTGAAGAGGTTGCTGCTGCTGCTG 1855
DB 1768 TGGTCCAAACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1827
QY 1856 CTGTGCGAAGCAGAGGTACGAGCAGATCGGGAAGCCAGCGCGCGCTGCTGCTGCTGCTG 1915
DB 1828 CTGTGCGAAGCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1887
QY 1916 CTGCGCTTCAATCCCAAGCGCTGAGCGGCTGCGGCGCGATTTGTGAACATGGAAGTCTG 1975
DB 1888 CTGCGTTTCAATCCCGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1947
QY 1976 GGAGCCAGAGATTTCCGAGAGAAAAAGAGGCGCGAGCGCTCTCACTCGAGGTTCAAGSCA 2035
DB 1948 GGTGCTGCTACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2007
QY 2036 CTGTTCAGCTGTCTAACTACGAGCGCGCGCGCGCGCGCGCTCTCTGCGCGCTCTGCTG 2095
DB 2008 CTGTCTCCGCTTCTGAACTACGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2067
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DB 2068 CTGGCTGTGAGACACATCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2127
QY 2156 GACCGCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGAGCGCGCTGCTGCTGCTGCTG 2215
DB 2128 GACCGCGCGCGGAACTGTACTTCTGTTAAAGTTGACGTTACCGCGCGCTGCTGCTGCTG 2187
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DB 2188 CCGCAGGACGCTGTGACCGAAGTATCGCTTCCATCATCAAAACCCAGAAACACCTACTG 2247
QY 2276 GTGCGTGGTATGCGGTGCTGCAAGCGCGCGCTGCGGACGCTGCGGAGGCGCTTCAAG 2335
DB 2248 GTTCTGCTTACGCTGTGTGTTTCAAGAGCTGCTCACGCTGCTGCTGCTGCTGCTGCTGCT 2307
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DB 2308 TCCACGCTTTCACCGCTGACCGACCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2367
QY 2396 CAGGAGACAGCGCGCTGAGGATGCGCTGCTATCGAGCAGAGCTCTCTCCCTGAAATGAG 2455
DB 2368 CAGGAAACCTCCCGCTGCTGAGCGCTGTTGTTATCGAACAGTCTCTCTCTCCCTGAAAG 2427
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DB 2428 GCTTCTCTCGGCTGTGTGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2487
QY 2516 AGGCGCAAGTCTTACGCTCCAGTCCAGGAGTCCCGAGGCTGCTGCTGCTGCTGCTGCTG 2575
DB 2488 CGTGTGTAATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2547
QY 2576 CTCTGAGCTGTGCTACGCGGAGATGGAGAAAGCTGTTTGGGGGATTCGCGGAGAC 2635
DB 2548 CTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2607
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Query Match 54.7%; Score 2196.6; DB 5; Length 3396; Best Local Similarity 77.9%; Pred. No. 0; Matches 2646; Conservative 0; Mismatches 749; Indels 0; Gaps 0;									
QY	56	ATGCGCGCGCTCCCGCTGCGAGCCGTGGGCTCCCTGCTGCGCAGCACTACCGCGAG	115	1076	CTGCGGCCCTCTTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGCGCTCGGAGGCTC	1135	QY	1076	CTGCGGCCCTCTTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGCGCTCGGAGGCTC
DB	1	ATGCGCGCGCGCGCGCTGCGCGGCTGCGCAGCTGCTGCGCAGCCATATCGCGAA	60	1021	CTGCGCCCGAGCTTCTGCTGAGCAGCCTGCGCGCAGGCTGACCGCGCGCGCGCTG	1080	DB	1021	CTGCGCCCGAGCTTCTGCTGAGCAGCCTGCGCGCAGGCTGACCGCGCGCGCGCTG
QY	116	GTGCTGCGCGTGGCACACTTCTGCGGCGCCTGCGGCCCCAGGGCTGCGGCTGCTGCAG	175	1136	GTGAGAGCACTTCTTCTGGGTTCAGGCCCTGGATGCCAGGACACTCCCGCAGGTGCGC	1195	QY	1136	GTGAGAGCACTTCTTCTGGGTTCAGGCCCTGGATGCCAGGACACTCCCGCAGGTGCGC
DB	1	ATGCGCGCGCGCGCGCTGCGCGGCTGCGCAGCTGCTGCGCAGCCATATCGCGAA	60	1081	GTGGAACCAITTTTCTGGGAGCGCGCGTGGATGCCGGGACCCCGCGCGCTCGCG	1140	DB	1081	GTGGAACCAITTTTCTGGGAGCGCGCGTGGATGCCGGGACCCCGCGCGCTCGCG
QY	176	GCGGGGACCGGGGCTTTCGCGCGCTGCTGCGGCCCCAGGGCTGCGGCTGCTGCAG	235	1196	GCGTGGCCCCAGCGCTACTGCAAAATGCGGCCCTGTTCTTGGAGCTCTTGGGAACCA	1255	QY	1196	GCGTGGCCCCAGCGCTACTGCAAAATGCGGCCCTGTTCTTGGAGCTCTTGGGAACCA
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QY	176	GCGGGGACCGGGGCTTTCGCGCGCTGCTGCGGCCCCAGGGCTGCGGCTGCTGCAG	235	1256	GCGCAGTCCCTACGGGGTGTCTCTCAAGACGACTGCGCGCTGCGGAGCTCGGCTCAC	1315	QY	1256	GCGCAGTCCCTACGGGGTGTCTCTCAAGACGACTGCGCGCTGCGGAGCTCGGCTCAC
DB	121	GCGCGATCCGGGGCTTTGCGCGCTGCTGCGGCCCCAGGGCTGCGGCTGCTGCAG	180	1201	GCGAGTCCCGGTATGGCTGTCTGAAACCCCATTTGCCGCTGCGCGCGGTGACC	1260	DB	1201	GCGAGTCCCGGTATGGCTGTCTGAAACCCCATTTGCCGCTGCGCGCGGTGACC
QY	236	GACGACGCGCGCGCGCGCGCTTCTTTCGCGCAGGTGCTGCTGCTGAAGAGCTG	295	1316	CCAGCAGCGGTGTCTGTGCCGGGAGAGCCACAGGGCTCTGTGGCGGCCCGCAGAG	1375	QY	1316	CCAGCAGCGGTGTCTGTGCCGGGAGAGCCACAGGGCTCTGTGGCGGCCCGCAGAG
DB	181	GATGCGCGCGCGCGCGCGCGAGCTTTCGCGCAGGTGCTGCTGCTGAAGAGCTG	240	1261	CCGGGGGGGGGTGTGCGCGCGGAAAAACCGCAGGCGAGGTGCGCGCGCGGAGAA	1320	DB	1261	CCGGGGGGGGGTGTGCGCGCGGAAAAACCGCAGGCGAGGTGCGCGCGCGGAGAA
QY	296	GTGGCCGAGTGTGCGAGAGCTGTGCGAGCGCGCGGCGAAGAGCTGCTGCGCTTCGCG	355	1376	GAGGACAGACCCCGCTCGCTGCGAGCTGTCTCCGCCACAGCAGACGCCCTTGGCAG	1435	QY	1376	GAGGACAGACCCCGCTCGCTGCGAGCTGTCTCCGCCACAGCAGACGCCCTTGGCAG
DB	241	GTGGCGCGTGTGCTGCGAGCGCTGTGCAAGCGCGCGCGGAAAAACGCTGCTGGC	300	1321	GAAGATACCGATCCGCGCGCTGTGTCAGCTGTCTGCGCAGCATAGCAGCCGCTGCGAG	1380	DB	1321	GAAGATACCGATCCGCGCGCTGTGTCAGCTGTCTGCGCAGCATAGCAGCCGCTGCGAG
QY	356	TTGCGCTGTGAGCGGGCGCGGGGCCCCCGAGGCTTACACACAGGTGCGC	415	1436	CTGTACGGCTTCTGCGGGCTGCTGCGCGGCTGTGCCCCAGGGCTCTTGGGGCTCC	1495	QY	1436	CTGTACGGCTTCTGCGGGCTGCTGCGCGGCTGTGCCCCAGGGCTCTTGGGGCTCC
DB	301	TTTGGCTGTGATGGCGCGCGCGCGCGCGCGGAAAGCTTTACCAACAGGTGCGC	360	1381	GTGTATGCTTTGTGCGCGCTGTGCTGCGCGCTGTGTGGCGGGCTGTGTGGGGCAGC	1440	DB	1381	GTGTATGCTTTGTGCGCGCTGTGCTGCGCGCTGTGTGGCGGGCTGTGTGGGGCAGC
QY	416	AGCTACTTGCACACCGTGTGACGACGCTGTGCGGGGAGCGGGGCTGGGGCTGCTG	475	1496	AGGCACACGACCGCGCTTCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGGAAGCAT	1555	QY	1496	AGGCACACGACCGCGCTTCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGGAAGCAT
DB	361	AGCTATCTGCGAACAACCGTACCGATGCGCTGCGCGCAGCGCGCTGGGCTGCTG	420	1441	CGCCATACGAACCGCGCTTCTGCGCAACACCAAAAAATTTATAGCCTGGGCAACAT	1500	DB	1441	CGCCATACGAACCGCGCTTCTGCGCAACACCAAAAAATTTATAGCCTGGGCAACAT
QY	476	CTGCGCGCGTGGCGAGCAGTGTGTTCACTTCTGCGCAGCGTGGCGCTCTTTGTG	535	1556	GCAAGCTCTCGCTGCGAGGCTGACGTGGAAGATGAGCGTGGGGGACTGCGCTTGGGTG	1615	QY	1556	GCAAGCTCTCGCTGCGAGGCTGACGTGGAAGATGAGCGTGGGGGACTGCGCTTGGGTG
DB	421	CTGCGCGCGTGGCGATGATGTCTGTTGATCTGCTGCGCGCTGCTGCGCTGCTTTGTG	480	1501	CGAAACTGAGCCTGCAGGAACTGACCTGSGAAATGAGCTGCGCGATTTGGCGCTGCTG	1560	DB	1501	CGAAACTGAGCCTGCAGGAACTGACCTGSGAAATGAGCTGCGCGATTTGGCGCTGCTG
QY	536	CTGTGCTCCAGTGGCGCTTACAGGTGTGCGGCGCGCTGTACACAGCTGCGCGCT	595	1616	GCGAGGACCCAGGGTTGGCTGTCTCCGCGCGCAGAGCACCGCTGCGTGAGAGATC	1675	QY	1616	GCGAGGACCCAGGGTTGGCTGTCTCCGCGCGCAGAGCACCGCTGCGTGAGAGATC
DB	481	CTGTGGCGCGAGTGGCGCTATCAGGTGTGCGGCGCGCTGCTGCTGCTGCTGCTGCTG	540	1561	GCGCAGCGCGCGGTGGCTGCTGCGCGCGGGAACATCGCTGCGGGAAGAAAT	1620	DB	1561	GCGCAGCGCGCGGTGGCTGCTGCGCGCGGGAACATCGCTGCGGGAAGAAAT
QY	596	GCCACTCAGGCGCGCGCGCGCACACGCTAGTGACCCCGGAGCGCTTGGGATGCGAA	655	1676	CTGCGCAAGTTCCTGCATGCTGATGAGTGTGACGTGCTGCGAGCTGCTCAGGTCTTTC	1735	QY	1676	CTGCGCAAGTTCCTGCATGCTGATGAGTGTGACGTGCTGCGAGCTGCTCAGGTCTTTC
DB	541	GCGACCAAGCGCGCGCGCGCATCGAGCGCGCGCGCGCGCTGGGCTGCGAA	600	1621	CTGCGCAATTTCTGCATTGCTGATGAGCGTGTATGTGTGGTGAAGTCTCTGCGCAGCTTT	1680	DB	1621	CTGCGCAATTTCTGCATTGCTGATGAGCGTGTATGTGTGGTGAAGTCTCTGCGCAGCTTT
QY	656	GCGCGCTGGAACATAGGTGAGGAGCGCGGGTCCCGCTGGGCTGCGAGCCCGGGT	715	1736	TTTTATGTACGGAGACACGTTTCAAAAGAACAGGTCTTTTTTCTACCGGAAGTGTCT	1795	QY	1736	TTTTATGTACGGAGACACGTTTCAAAAGAACAGGTCTTTTTTCTACCGGAAGTGTCT
DB	601	GCGCGTGGAAACCATAGCTGCGGAGCGGCGTGGCGCTGCGGCTGCGGCGCGCGC	660	1681	TTTTATGTACCGAAACCACTTTCAGAAAAACCGCTGTTTTTTTTATCGAAAAAGCTG	1740	DB	1681	TTTTATGTACCGAAACCACTTTCAGAAAAACCGCTGTTTTTTTTATCGAAAAAGCTG
QY	716	GCGAGGAGCGCGGGGAGTGCCAGCGGAAGTCTGCGGTTGCCAAGAGGCCAGGCGT	775	1796	TGGAGCAAGTTTGCAGCAATTTGAATCAGACAGCACTTGAAGAGGTGACGTGGGAG	1855	QY	1796	TGGAGCAAGTTTGCAGCAATTTGAATCAGACAGCACTTGAAGAGGTGACGTGGGAG
DB	661	GCGCGCGCGCGCGCGCGAGCGCGAGCGCGAGCTGCGCTGCGCAACGCGCGCGCGC	720	1741	TGGAGCAACTGCGAGCATTTGGCATTCGCCAGCATCTGAAACGCGTGCAGCTGCGCGAA	1800	DB	1741	TGGAGCAACTGCGAGCATTTGGCATTCGCCAGCATCTGAAACGCGTGCAGCTGCGCGAA
QY	776	GCGCTGCGCTGAGCGGAGCGGACGCGCGCTTGGGAGGGGTCTTGGGCGCACCCGCGC	835	1856	CTGTGGAAGCAGAGGTGAGGAGCGGAGCGAGCGCGCGCTGCTGACGTGCCAGA	1915	QY	1856	CTGTGGAAGCAGAGGTGAGGAGCGGAGCGAGCGCGCGCTGCTGACGTGCCAGA
DB	721	GCGCGCGCGCGAAGCGAAGCGACCCCGTGGGCGAGGCGAGCTGGGCGCATCCGGC	780	1801	CTGAGCGAAGCGGAAGTCCGCCAGCATCGCAAGCGCGCGCGCTGCTGACCAAGCGC	1860	DB	1801	CTGAGCGAAGCGGAAGTCCGCCAGCATCGCAAGCGCGCGCGCTGCTGACCAAGCGC
QY	836	AGGAGCGTGAACGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	895	1916	CTCGCTTATCCCAAGCCTGACGGGTGCGGCGATTGTGAACATGGATACGTGTGTGT	1975	QY	1916	CTCGCTTATCCCAAGCCTGACGGGTGCGGCGATTGTGAACATGGATACGTGTGTGT
DB	781	GCGACCGCGCGCGAGCGATTCGGGGCTTTTTCGTGTGTGTGTGTGTGTGTGTGTGT	840	1861	CTGCGCTTATTCGGAACCGGATGCGCGCGCGATTGTGAACATGGATATATGTGTGT	1920	DB	1861	CTGCGCTTATTCGGAACCGGATGCGCGCGCGATTGTGAACATGGATATATGTGTGT
QY	896	GAAGCACTCTTTTGGAGGTGCGCTCTCTGCGACGCGCGCACTCCCAACCATCTGGGC	955	1976	GGAGCCAGAGTTTCCGAGAGAAAAAGAGCGCGAGCGCTCTCACTCGAGGTGAAGCA	2035	QY	1976	GGAGCCAGAGTTTCCGAGAGAAAAAGAGCGCGAGCGCTCTCACTCGAGGTGAAGCA
DB	841	GAAGCGACCGCTTGAAGGCGCGCTGAGCGGCAACCGCCCATAGCCATCCAGGCTGGC	900	1921	GCGCGCGCACCTTTCGCGCGGAAAAACGCGCGGAACCGCTGACGAGCGGTGAAAGCG	1980	DB	1921	GCGCGCGCACCTTTCGCGCGGAAAAACGCGCGGAACCGCTGACGAGCGGTGAAAGCG
QY	956	GCGCAGCACCGCGGCGCGCGCATCCACATTCGCGGCGCACACGCTTCCCTGGGACACGCT	1015	2036	CTGTTCAGCGTGTCTAACTACAGCGGCGCGCGCGCGCGCGCTCTCTGGGCGCTCTGTG	2095	QY	2036	CTGTTCAGCGTGTCTAACTACAGCGGCGCGCGCGCGCGCGCTCTCTGGGCGCTCTGTG
DB	901	GCGCAGCATATCGGGCGCGCGCAGCACCGACCGCGCGCGCGCGCGCTGGGATACCCG	960	1981	CTGTTCAGCGTGTCTAACTACAGCGGCGCGCGCGCGCGCGCTCTCTGGGCGCTCTGTG	2040	DB	1981	CTGTTCAGCGTGTCTAACTACAGCGGCGCGCGCGCGCGCGCTCTCTGGGCGCTCTGTG
QY	1016	TGTCCCGGTGTACGCGGAGACCAAGCACTTCTACTCTCTACTCTCAGGGGAGAGAGAG	1075	2096	CTGGGCGTGGAGATATCCAGGGCTTGGGCGACCTTCTGTGTGTGTGTGTGTGTGTGTGT	2155	QY	2096	CTGGGCGTGGAGATATCCAGGGCTTGGGCGACCTTCTGTGTGTGTGTGTGTGTGTGTGT
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				2156	GACCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGCGCGGTACGACACCATC	2215	QY	2156	GACCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGCGCGGTACGACACCATC

[illegible]

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3181 GCGCGGGCCCCGCTCCGAGCGAAGCGGTGCAGTGGCTGTGCCATCAGC
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3356 AGCAGCTAGTCGAGAGCTCCGCGGGAGGAGCGTGTACTGCGCTGGAGG
3301 ACCAGCTGAGCGCAAACTGCGCGGCGACCACTCTGACCGGCTGGAAG
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RESULT 9
US-09-721-456-3
; Sequence 3, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

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QY 3538 GCCACACCCAGCCCGCAGCTGGAGTCTGAGGCTGAGTGAGTGTGGCCGAGGC 3597
Db 1679 GCCACACCCAGCCCGCAGCTGGAGTCTGAGGCTGAGTGAGTGTGGCCGAGGC 1738
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QY 3838 TCAGTGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGAATTTGGAGTGACCAAGGT 3897
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RESULT 10

US-09-721-456-266

: Sequence 266, Application US/09721456

: GENERAL INFORMATION:

: APPLICANT: Cech, Thomas R.

: Lingner, Joachim

: Nakamura, Toru

: Chapman, Karen B.

: Morin, Gregg B.

: Harley, Calvin B.

: Andrews, William H.

: TITLE OF INVENTION: Human Telomerase Catalytic Subunit

: NUMBER OF SEQUENCES: 727

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Townsend and Townsend and Crew LLP

: STREET: Two Embarcadero Center, Eighth Floor

: CITY: San Francisco

: STATE: California

: COUNTRY: USA

: ZIP: 94111-3834

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09721,456

: FILING DATE: 22-Nov-2000

: CLASSIFICATION: <Unknown>

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/974,549A

: FILING DATE: 19-Nov-1997

: APPLICATION NUMBER: US 08/724,643

: FILING DATE: 01-Oct-1996

: APPLICATION NUMBER: US 08/844,419

: FILING DATE: 18-Apr-1997

: APPLICATION NUMBER: US 08/846,017

: FILING DATE: 25-Apr-1997

: APPLICATION NUMBER: US 08/851,843

: FILING DATE: 06-May-1997

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: APPLICATION NUMBER: US 08/854,050
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: US 08/911,312
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: US 08/912,951
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: US 08/915,503
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: WO PCT/US97/17618
: FILING DATE: 01-OCT-1997
: APPLICATION NUMBER: WO PCT/US97/17885
: FILING DATE: 01-OCT-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Apple, Randolph Ted
: REGISTRATION NUMBER: 36,429
: REFERENCE/DOCKET NUMBER: 015389-002610US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 266:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2171 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 22..1716
: OTHER INFORMATION: /note= "EcoRI-NotI insert of
: clone 712562 encoding 63 kDa
: telomerase protein"
: SEQUENCE DESCRIPTION: SEQ ID NO: 266:
US-09-721-456-266
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Query Match 46.8%; Score 1877.2; DB 5; Length 2171;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 2140; Conservative 1; Mismatches 9; Indels 188; Gaps 7;

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Db 1 GCCAAGTTCCTGCACCTGGCTGATGAGTGTAGCTGCTGCAGGTCTTCTTT 60
QY 1739 TATGTACAGGAGACCACAGTTTCAAAAGAACAGAGCTCTTTTTCACCGGAAGAGTGTGG 1798
Db 61 TATGTACAGGAGACCACAGTTTCAAAAGAACAGAGCTCTTTTTCACCGGAAGAGTGTGG 120
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Db 361 TTCAGGCTGCTCAACTACGAGCGGCGCGGCCGCCCTGCTGAGGCTCTGTGCTG 420
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```


Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
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FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
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NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 641:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note= "hyrrf-encoding sequence employing alternative codon distributions for yeast (high expressing genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 641:
US-09-721-456-641

Query Match 43.7%; Score 1756; DB 5; Length 3396;
Best Local Similarity 69.8%; Pred. No. 0;
Matches 2371; Conservative 0; Mismatches 1025; Indels 0; Gaps 0;
US-09-721-456-641

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Db      1 ATCCCAAGAGCTCCCAAGATGTAGAGCTGTGTAGATCTTTGTGTAGATCTCCTACTACAGAGAA 60
QY      116 GTGCTGCCGTGGCCACAGTTCTGTGGCGCTGGCGCCCGCCAGGGCTGGGGCTGGTGCAG 175
Db      61 GTTTTGCATTTGGCTACTTTCGTAGAAAGATTGGGTCCCAAGAGTTGGAGATTGGTTCAA 120
QY      176 CGCGGGACCGCGCGCGCTTTCCCGCGCTGGTGGCCAGTGCCTGTGTGTGCTGCCCTG 235
Db      121 AGAGGTGACCCAGCTCTTTACAGACTTTGGTGTCTCAATGTTGTTGTTGTTCTCCATGG 180
QY      236 GAGCACGCGCGCGCGCGCGCTCTCTTCCCGCAGGTGCTCCCTCAAGAGAGCTG 295
Db      181 GACGCTAGACACACACAGCTGCTCCATCTTTCAGACAAAGTTTCTTTGTTGAAGAAATG 240
QY      296 GTGGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGCGGAGAACCTGTGGCGCTTCGGC 355
Db      241 GTTGCTAGAGTTTTCGCAAGATTGTGTGAAAGAGGTGCTTAAGAACGTTTGGCTTCGGT 300
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Db      301 TTGCGCTTGTGGAGCGTGTAGAGGTGCTAGAGGTGCTCCACAGAAAGCTTCTACTTCTGTAGA 360
QY      416 AGCTACTCTGCCAACACAGGTGACCGACGCTGCGGCGGAGCGGCGCGCGCGCGCTGCTG 475
Db      361 TCTTACTTGCACAAACACTGTTACTGACGCTTTGAGAGGTTCTGCTGCTGGGGTTGTTG 420
QY      476 CTGCGCGCTGGCGGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
Db      421 TTGAGAAGAGTTGTTGTCACGAGCTTTTGGTTTCACTTGTGGCTAGATGTGCTTTGTTGCTT 480
QY      536 CTGCTGCTGCCAGCTGCGGCTTACAGAGTGTGCGGCGCGCGCGCTGTACAGCTGCGCGCT 595
Db      481 TTGCTGCTCCATCTTGTGCTTACCAAGTTTGTGCTCCACATGTTACCAATTTGGTGTCT 540
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QY      656 CGGGCTTGAACCATAGCGTACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 715
Db      601 AGAGCTTGAACCATCTGTTAGAGAGCTGTTGTTTCCATTTGGGTTTGGCAGCTCCAGGT 660
QY      716 GCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 775
Db      661 GCTAGAAGAGAGGTGTTCTGCTTCTAGATCTTTGCCATTTGCCAAGAGAGACCAAGA 720
QY      776 GCGCTGCCCTGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 835
Db      721 GGTGCTGCTCCAGAACACAGAAAGAACTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
QY      836 AGGACGCTGGACCGAGTACCGTGTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
Db      781 AGAACTAGAGTCCATCTGACAGAGGTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY      896 GAAGCACCTCTTTGGAGGTTGGCTCTCTGGCACCGCGCGCGCGCGCGCGCGCGCGCGCG 955
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QY      956 CGCAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1015
Db      901 AGACAACACACGCTGCTCCATCTACTTCTAGACCAAGCAAGACCATGGGACACTCCA 960
QY      1016 TGTCCCGCGGTGACCGCGAGACCAAGACACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1075
Db      961 TGTCCACCAAGTTTACGCTGAACTAAGCACTTCTTGTACTCTTCTGTGTGTGTGTGTGTGT 1020
QY      1076 CTGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
Db      1021 TTGAGACCATCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
QY      1136 GTGGAGACCATCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1195
Db      1081 GTTGAACATATTTTCTTGGGTTCTTACCATGGATGCCAGGTACTCCAAAGAGATTGCCA 1140
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QY	1196	CGCCTGCCACGCGTACTGGCAAAATGGGCCCTGTCTTCGTGAGCTGCTTTGGGAACAC	1255
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QY	1256	CGCAGTGCCTTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCAGCTGGGTCAC	1315
Db	1201	GCTCAATGTCATACGGTGTTTCTTGAAGACTCACTGTCCATTGAGAGCTGCTGTACT	1260
QY	1316	CCAGCAGCGGTGCTGTGCCCGGGAGAACCCAGGCTCTGTGGCGGCCCGGAGAG	1375
Db	1261	CCAGTCTGTGTGTGTGTAGAGAAAAGCCACAAGTTCTGTGTCTCCAGAGAA	1320
QY	1376	GAGGACACAGACCCCTGCGCTGGTCCAGTGTCTCCGCCAGACACAGCCCTGGCAG	1435
Db	1321	GAGACACTGACCCCAAGAAGATTGGTTCAATGTGTGAGACAACACTCTTCTCATGGCAA	1380
QY	1436	GTGTACGGCTTGTGTCGGGGCTGCTCGCGCGGTGCTGCCCGACGACGCTCTGGGCTCC	1495
Db	1381	GTTTACGGTTTCGTTAGAGCTTGTTTGAAGATTTGGTCCACAGGTTTGTGGGTTCT	1440
QY	1496	AGGCACAACGACCGCGTCTCTCAGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT	1555
Db	1441	AGACACAACGAAGAAGATTTCTGAGAAACACTAAGAAGTTCATTTCTTTGGCTAAGCAC	1500
QY	1556	GCCAAAGCTTCGCTGCAGGAGCTGACGTGGAAGATGAGCTGCGGGAGTCGCTGGCTG	1615
Db	1501	GCTAAGTTGTCTTGTGCAAGAATTGACTTGGGAAGATGTCTGTAGAGACTGTGCTGGTTG	1560
QY	1616	CGCAGGACCGAGGGTGTGTTGCCGGCCGACAGACACGCTGCTGCGTAGGAGATC	1675
Db	1561	AGAAGATCTCCAGTGTGGTTGTGTCTCAGCTGCTGGAACACAGATTGAGAGAAGAAAT	1620
QY	1676	CTGCGCAAGTTCCTGCACTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGGCTTTTC	1735
Db	1621	TTGGCTAAGTCTTTCACCTGGTTGATCTCTGTTTACGTTCTTCAATTTGATCTTTTC	1680
QY	1736	TTTTATGTCAGGAGACCACTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGC	1795
Db	1681	TTCTACGTTTACTGAATCTTTTCCAAAGAACAGATTTGTCTCTACAGAAAGTCTGTT	1740
QY	1796	TGGAGCAAGTTGCAAGCACTTGAATTCAGACACACTTTGAAGAGGTGCAAGCTGCCGGAG	1855
Db	1741	TGGTCTAAGTTGCAATATTTGTTNTATGACACACTTTGAAGAGAGTTCAATTTGAGAGAA	1800
QY	1856	CTGTGGAAGCAGAGTCTAGCGACATTCGGGAAGCCAGGCCCGCTGTGAGCTCCAGA	1915
Db	1801	TTGTCTGAAGCTGAAGTTAGACAACACAGAGAAGCTTAGACCCTTTTGTGACTTCTAGA	1860
QY	1916	CTCGCTTCAATCCCAAGCCTGACGGCTGCGGCCGATTTGTGAACATGAGACTACGTCGTG	1975
Db	1861	TTGAGATTCAATCCAAAGCCAGACGGTTTGAGACCAATTTGTTAACTAGACTACGTTGTT	1920
QY	1976	GGAGCCAGAAGTTCCGACAGAGAAAAGGGCCGAGCTCTCACCTCGAGGTTGAAGGCA	2035
Db	1921	GGTGTAGAATTTTTCAGAGAGAAAAGAGCTTGAAGATTTGACTTCTAGAGTTAAGGCT	1980
QY	2036	CTGTTTCAGGCTGCTCAACTACGAGCGGGCGCGCCGCTCTCTGCGGCTCTGTG	2095
Db	1981	TTGTTCTCTGTTTGAATACGAAAGAGCTAGNAGACAGGTTTGTGGGTGCTTCTGTT	2040
QY	2096	CTGGGCCCTGAGATNATCACAGGGCCTGGCGACCTTCGTGCTGCGTGTGCGGGCCAG	2155
Db	2041	TTGGGTTTGGACACATTCACAGAGCTTGGAGAACTTTTCGTTTGAAGATTAGAGCTCAA	2100
QY	2156	GACCCGCGCTCTAGCTGTACTTTGTCAGAGTGGATGTACGGGGCCGTAACACACCATC	2215
Db	2101	GACCCACACAGAAATTGACTTCGTGTTAAGGTTGAGTTTACGTGCTTTACAGACTATT	2160
QY	2216	CCCCAGGACGGCTACGGAGGTCATCGCCAGCATCATCAAAACCCACAGAACAGTACTGC	2275
Db	2161	CCACAAGACAGATTGACTCAAGTTATTGCTTCTATTATTAAAGCCACAAAACACTTACTGT	2220

QY	2276	GTGCGTCGGTATGCGGTCCAGAAAGCGCCCATGGGACAGCTCCCAAGGCGCTTCAAG	2335
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QY	2336	AGCCACGCTCTACCTTGACAGAGCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTG	2395
Db	2281	TCTCAGGTTCCTACCTTTGACCTGTGCAACCATACATGACAGAAATTCGTGTGCTCACTTG	2340
QY	2396	CAGGAGACAGCCCGCTGAGGGATGCGGTCTCATCGAGCAGAGCTCCTCCCTGAAATGAG	2455
Db	2341	CAAGAAACTCTCCATTTGAGAGAGCGTGTGTATTGAACAACTCTCTTTTGAACGAA	2400
QY	2456	GCCAGCAGTGGCCTTCGACGCTTCTTCAAGCTTCATGTGCCACACGCGCTGCCATC	2515
Db	2401	GCTTCTTCTGTGTTGTCGACGTTTTCTTGAGATTCTATGTCACACGCTGTTAGAAAT	2460
QY	2516	AGGGCAAGTCTAGTCCAGTGGCCAGGGGATCCCGCAGGCTCCATCTCTCCAGCTG	2575
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QY	2576	CTCTCAGCCCTGTGCTACGGGACATGGAGAAACAGCTGTTGCGGGGATTCGCGGGAC	2635
Db	2521	TTGTGTTCTTTGTGTACGGTGACATGGAAACAAGTTGTCGTGTATTGAAGAGAC	2580
QY	2636	GGCTGCTCCTCGCTTGGTGGATGATTTCTTGTGTGTGACACTCACCTCACCCACGGG	2695
Db	2581	GCTTGTGTTGAGATTGGTTGACGACTCTCTTGTGTTTACTCCACACTTGACTCAGCT	2640
QY	2696	AAACCTTCCTCAGGACCTTGGTCGAGGTGTCCTTGAGTATGGCTGCGTGGTGAAGTGG	2755
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QY	2756	CGGAAGCAGTGTGTAACTTCCCTGTAGAAGACGAGCCCTGGTGGTGACGGCTTTTGTT	2815
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QY	2816	CAGATGCGGCGCCACGGCCTATCCCTGCTGGCGCTGCTGTGGATACCCGGACCCG	2875
Db	2761	CAAAATGCCAGCTCACGGTTGTCCCATGGTGGTTGTTGTTGGACACTGAACACTTG	2820
QY	2876	GAGGTGAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGAGTCTCACCTTC	2935
Db	2821	GAGGTCAATGTGACTACTCTCTTACGGCTAGAACTTCTATTAGAGCTCTTTTGACTTTC	2880
QY	2936	AACCGCGCTTCAAGCTGGGAGAACATCGCTCGCAACTCTTTGSGGTCTTGGCGCTG	2995
Db	2881	AACAGAGGTTCAAGCTGGTAGAACATGAGAAGAAAGTTGTTCCGGTGTTTGAGATTG	2940
QY	2996	AAGTGTACAGCCTGTGTTCTGGATTTGAGGTGAACGCTCCAGACGGTGTGCACCAAC	3055
Db	2941	AAGTGTCACTCTTTGTTCTTGGACTTGCAGTTAACTCTTTGCAAACTGTTGTACTAAC	3000
QY	3056	ATCTACAAGATCTCTGCTGCGAGGCTACAGGTTTCACGCAFGTGTGTGAGCTCCCA	3115
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Db	3061	TTCCACCACAAGTTTGGAGAAGCCCACTTCTTCTTGAGAGTTATTCTGACACTGCT	3120
QY	3176	TCCCTCTGCTACTCCATCTTGAAGCGCAAGACGAGGATGTGCTGGGGGCCAAGGCG	3235
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QY	3236	CGCGCGGCGCCTGTGCCCTCCGAGGCGGTGAGTGCTGTGCCACCAAGATTCCTGCTC	3295
Db	3181	GCTGCTGGTCCATTGCCATCTGAAGCTGTTCATATGGTTGTGTGCACCAAGCTTCTTGTG	3240
QY	3296	AAGCTGACTCGACACGCTGTCACTACGTGGCACTCTCGGGCTCACTCAGGACAGCCAG	3355
Db	3241	AAGTTGACTAGACACAGAGTTACTTACGTTTCCATTTGTTGGGTCTTTTGAAGAATGCTCAA	3300
QY	3356	ACCGAGCTGAGTCGGAAGCTTCCCGGGGAGGAGCGCTGACTGCCCTGGAGGCGCCAGCAAC	3415

Db 3301 ACTCAATTGCTAGAAAGTGGCAGGTACTACTTGTGACTGCTTGGAAAGTGTGCTAAC 3360
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RESULT 13
PCT-US03-19844-5
; Sequence 5, Application PC/TUS0319844
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Majumdar, Anish Sen
; APPLICANT: Ferber, Iris
; APPLICANT: Frolkis, Maria
; APPLICANT: Wang, Zhuo
; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Reverse Transcriptase
; FILE REFERENCE: 086/200
; CURRENT APPLICATION NUMBER: PCT/US03/19844
; PRIOR FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/393,295
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4170
; TYPE: DNA
; ORGANISM: Mesocricetus auratus
PCT-US03-19844-5

Query Match 41.6%; Score 1670.6; DB 1; Length 4170;
Best Local Similarity 69.7%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 964; Indels 90; Gaps 8;

QY 52 CGCGATGCGCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGGAGCCACTACCG 111
Db 24 CGGATGCGCGCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGGAGCCACTACCG 83

QY 112 CGAGGTGCTGCGCTGCGGACGCTTCTGCGGCGCTGCGGCGCGCGGCTGCGGCGTGT 171
Db 84 TCAGGTGCTGCGCTGCGGACGCTTCTGCGGCGCTGCGGCGCGCGGCTGCGGCGTGT 143

QY 172 CGAGCGCGGCGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGTGT 231
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QY 232 CTGGGACG 291
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QY 292 GCTGCTGCGCGCGCTGCTGCGAGGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCT 351
Db 264 GCTGCTGCGCGCGCTGCTGCGAGGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCT 323

QY 352 CGGCTTGGCGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 411
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QY 412 GCGCAGCTACTCTCCCAACAGCTGACCGAGCGCTGCGGCGCGCGCGCGCGCGCGCGCT 471
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QY 472 GCTGCTGCGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 531
Db 444 TCTGCTGAACGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTAA 503

QY 532 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
Db 504 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563

QY 592 CGCTGCCACTCAGGC-----CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAG 627

Db 564 TGCACCGGAGAAACCTGGCCTTCTGTGTCCCGCATCTACAGGCCACACGACCGCTGGG 623
QY 628 TGGACCCCGAAAGCGCTGTGGATGC---GAACCGGCGCTTGGAAACCATAGCGTCAGGCG 684
Db 624 CAGAAATTTTACTCATCTTGGATCCACACACCGGTCAGGAACAGCAGTCAACAGNAGC 683
QY 685 CGGGGTCCCGCTGGCGCTGCGAGCGCGGCTGCGAGGAGCGCGGGGAGTGCACGCG 744
Db 684 ATGGAACCCCGCGCTTGGCATCTCGAGAGCGGAGCGAGTCTAAGCATCAACCAATAG 743
QY 745 AGTCTGCGGCTTGGCCAAAGAGCGCGAGGCTGCGCTGCGCTGAGCCGCGGAGCGCGC 804
Db 744 AGTGTGCTTCCATCTAAGAAGCGCGAGTGTGGCGCCCGAGACTGGAGAAGGAGCC 803
QY 805 CGTTGGCCAGGGTCTCTGGCGCCACCGCGGCGAGGCGGCTGGACCGAGTGCACGCTGTT 864
Db 804 CTACAGCGAGCGATTTCCAAACCCATCAGACAAACATGGTGCCAAATCTTCCCAAGTC 863
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QY 985 ATCGCGCGCACACACGCTCCCTGGGACACGCTTCTCCCGCGGTGTACCGGAGACCAAGCA 1044
Db 978 CTTGAGTACCACTGTGCCAAATGCTTTCAGCTCAGACCAATATATAGAGACCAACG 1037
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Db 1038 CTTCTCTACTCTAGGAAAGTGGCGGAGAGGCTGAACCCCTCTCTTCTACTCAACA 1097
QY 1102 TCTGAGCGCGCACTGCTGCGCTGCGAGGCTGCTGGAGACCATCTTCTTGGGTTCCAG 1161
Db 1098 CTTGAGCGCGCACTGCTGCTGCGGCGGAGAGCTGGTAGATATCTTCTTAGGCATGAG 1157
QY 1162 GCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCGCTGCCCGACCGCTTACTTGGCAAT 1221
Db 1158 ACCTAGGACATCGGACCACTCTGTGGAGACCGCGCTATCAGAGCGCTACTTGGCAGAT 1217
QY 1222 GCGGCGCTGCTTCTGAGCTGCTGGGAAACACAGCGGAGTGCCTTACGGGCTGCTCT 1281
Db 1218 GCGGCGCTTATTCAGCAGTGTCTGTGAACCATGCGCGCTGCTATGCGGCTCT 1277
QY 1282 CAAGCGCACTGCGCGCTGCGAGCTGCGGTCACCCAGCAGCGGCTGCTGTGCGCGGGA 1341
Db 1278 CAGTCCATTTGAGGTTTCGGACCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCT 1327
QY 1342 GAAGCCCGAGGCTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCT 1401
Db 1328 -----TGAACACCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCT 1355
QY 1402 GAGCTGCTCGCT 1461
Db 1356 GAATTTTCTGCTGCTTACACAGCAGTCCCTGGCAGTATATGGCTTTCTTTCAGGCTGT 1415
QY 1462 GCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCT 1521
Db 1416 CGAAAGCTGCTGCTGCGGCTCTGCGGCTTCCCGCGCGCGCGCGCGCGCGCTTCTTAA 1475
QY 1522 GAACACCAAGAGTTCATCTCCCTGGGAAAGCATGCAAGCTCTGCTGCGAGGCTGAC 1581
Db 1476 GAGCTGAGCGGCTTCTCTCTTGGGAAAGTATGACAGCTCTGCTGCGAGGCTGAC 1535
QY 1582 GTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGGAGAGCGCGCGCGCTGCTGCT 1641
Db 1536 GTGGAAGATGAAAGTTCAAGACTGCGAGTGGCTTGGCAGCAGCGCGCGCGCGCGCTGCT 1595
QY 1642 TCCGCGCGCGAGACCGCTGCTGAGGAGATCTTGGCGCAAGTCTTCTGCGAGCTGAT 1701

Query Match 39.9%; Score 1600.8; DB 1; Length 3426; Best Local Similarity 68.9%; Pred. No. 0; Matches 2379; Conservative 0; Mismatches 967; Indels 108; Gaps 9;		
QY	40	CCCGCCACCCCGCGATGCGCGCTCCCGCTCCCGCTGCGAGCGTGCCTCCTGCTGG 99
DB	14	CCCGCCCTTGACACATGACACCGCGCTCCTCGTTGCCCGCGGTGCGCTCTCTGCTGG 73
QY	100	CAGCCACTACCGGAGTGTCTCCGCTGGCCACGTTGCTGCGCGCCCTGGGCGCCACAGG 159
DB	74	CAGCCGATACGGGAGGTGTGCGCGCTGCGCAACCTTTGTGCGCGCTGGGCGCCGAGG 133
QY	160	CTGGGGCTGTGTCAGCGGGGACCGCGCGCTTTCGGCGCGCTGGTGGCCAGTGCCCT 219
DB	134	CAGGGCGCTTGTGCAACCGGGGACCGGAAGATCTACCGCACTTTGGTTGCCCAATGCC 193
QY	220	GGTGTGCGTGGCTGGGAGCAGCGCGCGCCCGCGCGCCCTCTCTTCGCGCAGGTGTC 279
DB	194	AGTGTGATGACTGGGGCTCAGCGCTCCACCTGCCGACCTTTCTTCCACGAGGTGC 253
QY	280	CTGCCGTGAAGAGCTGGTGGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCCGAAGAA 339
DB	254	ATCCCTGAAGAGCTGGTGGCCAGGTTGTGTCAGAGACTCTCGGAGCGCAACAGAGAA 313
QY	340	CGTGTGCGCTTCGGGTTGCGCGTGTGTCAGCGGGGCGCGGGGGCCCCCGAGGCGCTT 399
DB	314	CGTGTGCGCTTTGGCTTTGAGCTGCTTAACGAGGCCAGAGCGGGCGCTTCCCATGGCCT 373
QY	400	CACCAACGAGCGCGCACTCTCCCAACAGGTGACCGACGCACTGCGGGGAGCGG 459
DB	374	CACTAGTGGTGGTGTGCTTCTGCCCAACTGTATTGAGACCTCGGTGTGTCAGTGG 433
QY	460	GGCGTGGGGCTGCTGCTGCGCGGTGGGCGACGACGTGCTGTTCACTGCTGGCAG 519
DB	434	TGCATGGATGCTACTGTTGAGCGGAGTGGGCGACGACCTGCTGGTCACTGCTGCGACA 493
QY	520	CTGGCGGCTTTGTGCTGGTGGCTCCGAGCTGCGGCTACGAGGTGTGCGGGCGCGCT 579
DB	494	CTGTGCTCTTTATCTTGTGGTGGCGCCGAGCTGTGCGCTACCAAGGTGTGGGTCTCCCT 553
QY	580	GTACCAGCTTCGGCGCTGCCACTCAGCGCCGCGCGCGCCGACACGCTAGTGGACCCGGA 639
DB	554	GTACCAAAATTTTGCCACACCGGATATCTGGCCCTCTGTGCTCGCTAGTTACAGGCCAC 613
QY	640	GGTCTGGGATGC-----GAACGGGCGTGGAAACCATAG 672
DB	614	CGGACCGGTGGCAGGAATTTCACTAACTTAGGTTCTTTACAACAGATCAAGAGCAGTAG 673
QY	673	CGTCAGGGAGCGGGGTCCCGCTGGGCTGCCAGCCCGGCTGGGAGGCGGGGG 732
DB	674	TCGCCAGGAAGACCCGCTGGCCCTTGCCATCTCGAGGTACAAAGAGGCATCTGAG 733
QY	733	CAGTGCAGCCGAAGTCTCGCGTTGCCAAGAGGCCAGCGCTGGCGCTGCCCTGAGCC 792
DB	734	TCTCACCAGTACAGTGTGCTTACGCTAAGAAGGCCAGTGTATCTCTCTCCGAGAT 793
QY	793	GGAGCGGAGCGCGGTTGGCAGGGTCTCTGGGCCACCGCGGCGAGCAGCGTGGACCGAG 852
DB	794	GGAGGAGGAGCCCCACAGCAGGTGCTACCAACCCCATCAGGCAATCATGGTGGCCAAG 853
QY	853	TCACCGTGTGTTCTGTGTGGTGTACCTGCCAGACCCCGCGGAAGAACCATCTTTTGA 912
DB	854	TCTGTCTGCTCCCGGAGTGCCTACT-----GCAGAGAAAGATTTGTCTTCTAA 904
QY	913	GGTGGGCTCTCTGGCAGCGCACTCCCAACCATCCGTGGGCGCCGACCAACCGCGG 972
DB	905	AGGAAGGTGTCTGACCTGAGTCTCTCTG---GGTGGGTGTGCTGTAAACAACAGCCCA 961
QY	973	CCCCCATCCATCGCGGCCACCACTGCTCTGGGACAGCGCTTGTCCCGCGGTGTACGC 1032
DB	962	CTCCACAT---CTCTGCTGACCAACCCCGGCCCAAAATGCTTTTCAGCTCAGGCCATTTAT 1018
QY	1033	CGAGACCAGGACTTCTCTACTCTCTCAGGCGA---CAAGGAGCAGCTGCGGGCCCTCTT 1089
DB	1019	TGAGACACGACATTTCTCTTACTCCAGGGAGATGGCCAAGCGCTTAAACCCCTCATTT 1078
QY	1090	CTACTCAGCTCTCTGAGGCCAGCTGACTGCGCTCGAGGCTCGTGAGACCATCTT 1149
DB	1079	CTACTCAGCAACCTCCAGCCTTAATTTGACTGGGCCAGGAGACTGGTGAGATCATCTT 1138
QY	1150	CTTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCAGGTTGCCCGCTGCCCCAGG 1209
DB	1139	CTTGGGCTCAAGGCCCTAGGACATCAGGACCACTGTCAGAGACACACCGCTCTATCGGCTG 1198
QY	1210	CTACTGGCAAAATGCGGCCCTGTCTTCTGAGCTGCTTGGGAACCAAGCGAGTGGCCCTA 1269
DB	1199	ATACTGGCAGATGCGGCCCTGTTCACACAGCTGCTGGTGAACCATGCAAGTGGCAATA 1258
QY	1270	CGGGTGTCTCTCAAGACCACTGCGCGTGGAGCTGCGGTACCCCAAGCAGCGCGTGT 1329
DB	1259	TGTCAGACTCTCAGGTCACTTTGACGTTTGAACAGCAAAACCAACAGGTGACAGATGC 1318
QY	1330	CTGTGCCCGGGAGAGCCCGAGGCTCTGTGGCGGCCCGCGAGGAGGAGGACACAGACCC 1389
DB	1319	CT-----TGACACACAGGCC 1333
QY	1390	CGGTGCCCTGTGTCAGCTGCTCCGCCAGCACACAGACCCCTGGCAGGTGTACGGCTTCGT 1449
DB	1334	ACCGCACTTATGGAATTTGCTCGGCTGCACAGCAGTCCCTGGCAGGTATATGTTTCT 1393
QY	1450	GGGGCTGCTGCGCGCGCTGTCGCCCGCAGGCTGCGGCTCAGGACACACCAAGC 1509
DB	1394	TGGGCTGTCTCTGCAAGGTGTGCTGTCTGTCTCTGGGTACCGACACAAATGAGG 1453
QY	1510	CGCTTCTCTAGGACACCAAGAAATTCATCTCCCTGGGGAAGCATGCGCAAGTCTCGCT 1569
DB	1454	CGCTTCTTAAAGAACTTAAAGAAATTCATCTCGTTGGGGAATACGCAAGCTATCACT 1513
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; Sequence 640, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721.456
; FILING DATE: 22-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 640:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note= "hTERT-encoding sequence employing
alternative codon distributions for
yeast (all genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 640:
US-09-721-456-640

Query Match 38.4%; Score 1542.2; DB 5; Length 3396;
Best Local Similarity 65.9%; Pred. No. 0;
Matches 2237; Conservative 0; Mismatches 1158; Indels 0; Gaps 0;

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116 GTGCTGCCCTGCGCACAGTTCCTGCGGCGCTGCGGCGCCAGCGCTGGCGGTGGTCAG 175
61 GTTTTGCCATTGGCTACTTTGTAGAGATTGGTCCACAAGTTGGAGATTGGTTCAA 120

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121 AGAGGTGATCCAGCTGCTTTTAGAGCTTTTGGTTGCTCAATGTTGGTTGTCTCCATGG 180

236 GACGACGCGCGCGCGCGCGCTCCTTCCGCGAGGTGCTGCTGCTGCTGAAGAGCTG 295
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296 GTGGCCGAGTCTGCAGAGGCTGTCGAGCGCTGTGGCGCGCGGCGAAGCTGCTGCC 355
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416 AGCTACCTCCCAACAGCTGACCGACGCTGCGGCGGAGCGGCGGTGGGCGCTGCTG 475
361 TCTTATTGCGCAAACTACTGTTACTGATGCTTTGAGAGTCTGCTGCTGCTGCTGCTG 420

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421 TTGAGAAGAGTTGGTGATGATGTTTGGTTCAATTTGTTGGCTAGATGCTGTTGTTGTT 480

536 CTGGTGGCTGCCAGCTGGCGCTTACCAGTGTGCGGGCGCGCGCTGTACAGCTCGCGCT 595
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Job time : 935 secs


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ALIGNMENTS

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; Sequence 3, Application PC/TUS0115774
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancevicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0568
; CURRENT APPLICATION NUMBER: PCT/US01/15774
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
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Best Local Similarity 100.0%; Pred. No. 0;

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Db	961	GCACCGCGGGCCCCCATCCACATCGGGGCCACACAGTCCCTCGGACACGCTTGTTC	1020
Qy	1021	CCGGGTGACGGGAGACCAAGCACATCTCTACTCTCTAGGCGACAAGGAGCAGTGG	1080
Db	1021	CCGGGTGACGGCGAGACCAAGCACATCTCTACTCTCTAGGCGACAAGGAGCAGTGG	1080
Qy	1081	GCCTCCTCTTCTACTCAGCTCTCTGAGGGCCAGCCTGACTTGGCGCTCGGAGGCTCGTGA	1140
Db	1081	GCCTCCTCTTCTACTCAGCTCTCTGAGGGCCAGCCTGACTTGGCGCTCGGAGGCTCGTGA	1140
Qy	1141	GACCATCTTCTTGGGTTCAGGCCCTTGATGTCAGGGACTCCCGAGGTTCGCCGCGCT	1200
Db	1141	GACCATCTTCTTGGGTTCAGGGCCCTTGATGCCAGGACTCCCGCAGGTTCGCCGCGCT	1200
Qy	1201	GCCACGCGCTACTGGCAATCGGGCCCTGTCTTCTGGAGCTGCTTGGGAACACCGCA	1260
Db	1201	GCCACGCGCTACTTGGCAATCGGGCCCTGTCTTCTGGAGCTGCTTGGGAACACCGCA	1260
Qy	1261	GTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTCGAGCTCGGCTCACCCAGC	1320
Db	1261	GTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTCGAGCTCGGCTCACCCAGC	1320
Qy	1321	AGCCGGTGTCTGTCGCCGGAGAAAGCCAGGCTCTGTGGCGGCCCGCAGGAGGA	1380
Db	1321	AGCCGGTGTCTGTCGCCGGAGAAAGCCAGGCTCTGTGGCGGCCCGCAGGAGGA	1380
Qy	1381	CACAGACCCCGCTGCTGTCAGCTGCTCCGCCAGCACAGAGCCCTTGGCAGTGTA	1440
Db	1381	CACAGACCCCGCTGCTGTCAGCTGCTCCGCCAGCACAGAGCCCTTGGCAGTGTA	1440
Qy	1441	CGGCTTCTGCGGGGCTCGCTGCGCGCGCTGGTGCCTCAGGCTCTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCTGCGGGGCTCGCTGCGCGCGCTGGTGCCTCAGGCTCTGGGGCTCCAGGCA	1500
Qy	1501	CACGAAGCGGCTTCTCAGGAACACCAAGAAGTTCATCTCCTGGGAAGCATGCCAA	1560
Db	1501	CACGAAGCGGCTTCTCAGGAACACCAAGAAGTTCATCTCCTGGGAAGCATGCCAA	1560
Qy	1561	GCCTCCTGCGAGGCTGACGTGGAAGATGACGCTGCGGACTGCGCTGGCTGGCGCAG	1620
Db	1561	GCCTCCTGCGAGGCTGACGTGGAAGATGACGCTGCGGACTGCGCTGGCTGGCGCAG	1620
Qy	1621	GAGCCAGGGTGGCTGTCTCCGGCCGAGACACCGTCTCGTGAGGAGATCCTGGC	1680
Db	1621	GAGCCAGGGTGGCTGTCTCCGGCCGAGACACCGTCTCGTGAGGAGATCCTGGC	1680
Qy	1681	CAAGTTCCTGCACTGGCTGATGATGTACGTGCGAGCTGCTCAGGTCCTTTCTTTA	1740
Db	1681	CAAGTTCCTGCACTGGCTGATGATGTACGTGCGAGCTGCTCAGGTCCTTTCTTTA	1740
Qy	1741	TGTCACGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTCTCTGGAG	1800
Db	1741	TGTCACGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTCTCTGGAG	1800
Qy	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCGAGCTCGGAGCTGTC	1860
Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCGAGCTCGGAGCTGTC	1860
Qy	1861	GGAAGCAGAGGTTCAGGAGCATCGGGAAGCCAGGCCCGCCTGCTACGCTCCAGACTCCG	1920
Db	1861	GGAAGCAGAGGTTCAGGAGCATCGGGAAGCCAGGCCCGCCTGCTACGCTCCAGACTCCG	1920
Qy	1921	CTTCATCCCCAAGCCTCAGCGGCTGCGGCGGATGTGAACATGGACTACGCTCGTGGAGC	1980
Db	1921	CTTCATCCCCAAGCCTCAGCGGCTGCGGCGGATGTGAACATGGACTACGCTCGTGGAGC	1980
Qy	1981	CAGAACCTTCGCGAGAGAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTGT	2040
Db	1981	CAGAACCTTCGCGAGAGAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTGT	2040
Qy	2041	CAGCGTGTCTCACTACGAGCGGGCGCGGCCCGCGGCTCTCTGGGCGGCTCTGTGTGGG	2100

[illegible]

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Db 3121 TCAGCAAGTTTGGAGAACCCACATTTTCTCGCGCTCATCTCTCACAGGCGCTCCCT 3180
Qy 3181 CTGCTACTCATCTGAAAGCCAGAACGAGGATGTCTGGGGGCCAAGGGCGCGC 3240
Db 3181 CTGCTACTCATCTGAAAGCCAGAACGAGGATGTCTGGGGGCCAAGGGCGCGC 3240
Qy 3241 CGGCGCTCTGCCCTCCAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
Db 3241 CGGCGCTCTGCCCTCCAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
Qy 3301 GACTCGACACCGTGTCACTACCTACCTGACCTCCCTGGGGTCACTAGGACAGCCAGAGCGCA 3360
Db 3301 GACTCGACACCGTGTCACTACCTACCTGACCTCCCTGGGGTCACTAGGACAGCCAGAGCGCA 3360
Qy 3361 GCTGAGTGGGAAGTCCCGGGGAGACGCTGACTGCTGCTGAGGCGCGAGCCAGCAACCCGGC 3420
Db 3361 GCTGAGTGGGAAGTCCCGGGGAGACGCTGACTGCTGCTGAGGCGCGAGCCAGCAACCCGGC 3420
Qy 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTGTGATGGCCACCCGCCACAGCCAGGCGCA 3480
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTGTGATGGCCACCCGCCACAGCCAGGCGCA 3480
Qy 3481 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTAGCTCCAGGAGGAGGGCGCGCC 3540
Db 3481 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTAGCTCCAGGAGGAGGGCGCGCC 3540
Qy 3541 CACACCGAGGCGCGCAGCGTGGAGTCTGAGGCTGAGTGTGCTGGCGAGGCGCTG 3600
Db 3541 CACACCGAGGCGCGCAGCGTGGAGTCTGAGGCTGAGTGTGCTGGCGAGGCGCTG 3600
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Db 3601 CATCTCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTCCAGGCGCAAGGCT 3660
Qy 3661 GAGTGTCCAGCACACCTCGCGTCTTCACTTCCCGCACAGGCTGGCGCTCGGCTCCACCCCA 3720
Db 3661 GAGTGTCCAGCACACCTCGCGTCTTCACTTCCCGCACAGGCTGGCGCTCGGCTCCACCCCA 3720
Qy 3721 GGGCGAGCTTTCTCAGCAGGAGCGCGGCTTCCACTCCCGACATAGAGATAGTCCATCC 3780
Db 3721 GGGCGAGCTTTCTCAGCAGGAGCGCGGCTTCCACTCCCGACATAGAGATAGTCCATCC 3780
Qy 3781 CCAGATTGCGCATTTTACCCCTCGCCCTGCGCTTCCCTTCCAGCCCGCCACCATCC 3840
Db 3781 CCAGATTGCGCATTTTACCCCTCGCCCTGCGCTTCCCTTCCAGCCCGCCACCATCC 3840
Qy 3841 AGTGGAGACCTTGAGAGGACCTGGAGCTCTGGAAATTGGAGTGTGACCAAGAGTGTG 3900
Db 3841 AGTGGAGACCTTGAGAGGACCTGGAGCTCTGGAAATTGGAGTGTGACCAAGAGTGTG 3900
Qy 3901 CCCTGTACAGCGGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATGGGG 3960
Db 3901 CCCTGTACAGCGGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATGGGG 3960
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; Sequence 1, Application PC/TUS0231635
; GENERAL INFORMATION:
; APPLICANT: Boston University et al.
; TITLE OF INVENTION: PREADIPOCYTE CELL STRAINS AND USES THEREFORE
; FILE REFERENCE: BUI-011PC
; CURRENT APPLICATION NUMBER: PCT/US02/31635
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327650
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/327651
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-31635-1

Query Match 100.0%; Score 4015; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAGCCCTGGCCCGCCGCGCCGCGGATGCC 60
Qy 61 GCAGCGTCTCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
Db 61 GCAGCGTCTCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
Qy 121 GCAGCTGGCCACAGTTCGTGCGGCGCTGCGGCGCCCGCCAGGCTGGGGCTGTGTGACGCGGG 180
Db 121 GCAGCTGGCCACAGTTCGTGCGGCGCTGCGGCGCCCGCCAGGCTGGGGCTGTGTGACGCGGG 180
Qy 181 GGACCCGCGCGCTTTCCGCGCGCTGCTGCTGCGCAGTGTGCTGCTGCGCTGCGCTGGGACGC 240
Db 181 GGACCCGCGCGCTTTCCGCGCGCTGCTGCTGCGCAGTGTGCTGCTGCGCTGCGCTGGGACGC 240
Qy 241 ACAGCGCCCGCCCGCCCGCCCGCTTCCCTCCGCGCAGGTGTCTGCTGAAGAGCTGTGGTGC 300
Db 241 ACAGCGCCCGCCCGCCCGCCCGCTTCCCTCCGCGCAGGTGTCTGCTGAAGAGCTGTGGTGC 300
Qy 301 CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGGCTTCGC 360
Db 301 CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGGCTTCGC 360
Qy 361 GCTGCTGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGGCTTCGC 420
Db 361 GCTGCTGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGGCTTCGC 420
Qy 421 CCTGCCCAACACAGGTGACGACGACCTGCGGCGGAGCGGGCGCTGTGCTGCTGCTGCTGCTGCTG 480
Db 421 CCTGCCCAACACAGGTGACGACGACCTGCGGCGGAGCGGGCGCTGTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CCGCGTGGCGGAGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 CCGCGTGGCGGAGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 541 GGGTCCCGAGCTGGCGCTTACAGAGTGTGCGGCGCGCGCGCTGTACAGCTCGCGCTGGCCAC 600
Db 541 GGGTCCCGAGCTGGCGCTTACAGAGTGTGCGGCGCGCGCGCTGTACAGCTCGCGCTGGCCAC 600
Qy 601 TCAGGCGCGCGCGCGCGCGCGCGCTAGTGGACCGCGAGGCGCTGTGGGATGCGAAGCGGC 660
Db 601 TCAGGCGCGCGCGCGCGCGCGCGCTAGTGGACCGCGAGGCGCTGTGGGATGCGAAGCGGC 660
Qy 661 CTGGAACCATAGAGTCAAGGAGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 720
Db 661 CTGGAACCATAGAGTCAAGGAGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 720
Qy 721 GAGCGCGGGGCGAGTGCACGCGCGAGTGTGCGCGCTTCCCGAGGCGCGCGCGCGCGCGCGCGCGCG 780
Db 721 GAGCGCGGGGCGAGTGCACGCGCGAGTGTGCGCGCTTCCCGAGGCGCGCGCGCGCGCGCGCGCGCG 780
Qy 781 TGCGCGTGGCGGAGCGCGCGCGCTTGGGAGGCGGTCTCTGGGCCCGCGCGCGCGCGCGCGCGCGCG 840
Db 781 TGCGCGTGGCGGAGCGCGCGCGCTTGGGAGGCGGTCTCTGGGCCCGCGCGCGCGCGCGCGCGCGCG 840
Qy 841 GCGTGGACCGAGTCAAGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCGTGGACCGAGTCAAGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 CACCTCTTTGGAGGCTGCGCTCTCTGCGAGCGCGCACTCCCGCCATCCGCTGGCGCGCGCA 960
Db 901 CACCTCTTTGGAGGCTGCGCTCTCTGCGAGCGCGCACTCCCGCCATCCGCTGGCGCGCGCA 960
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Db	901	CACCTCTTTGGAGGTTGGCTCTCTGGACGGCGCCACTCCACCCCATCCGTGGCGCCGCA	960	Qy	2041	CAGGTGCTCAACTACGAGCGGGCGGCGCCCGGCTCTTGGGCGCCTCTGTGTGGG	2100
Qy	961	GCACACGGGGGGCCCCATCCATCAGTCGCGGGCCACGACGTCTCTGGACACGCTTGTC	1020	Db	2041	CAGGTGCTCAACTACGAGCGGGCGGCGCCCGGCTCTTGGGCGCCTCTGTGTGGG	2100
Db	961	GCACACGGGGGGCCCCATCCATCAGTCGCGGGCCACGACGTCTCTGGACACGCTTGTC	1020	Qy	2101	CTTGGAGGATATCCACAGGGCCCTGGCGCACCTTCGTGCTCGGTGCTGGGGCCACGACC	2160
Qy	1021	CCGGGTGAGCGGAGACCAAGACATTCCTCTACTCTCAGGGGACACAGGAGCAGCTGG	1080	Db	2101	CTTGGAGGATATCCACAGGGCCCTGGCGCACCTTCGTGCTCGGTGCTGGGGCCACGACC	2160
Db	1021	CCGGGTGAGCGGAGACCAAGACATTCCTCTACTCTCAGGGGACACAGGAGCAGCTGG	1080	Qy	2161	GC CGCCTGAGCTGTACTTTTGTCAAGGTGGATGTGACGGGCGCGTACACACCATCCCCCA	2220
Qy	1081	GCCTCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTTGGCGCTCGGAGGCTCGTGGA	1140	Db	2161	GC CGCCTGAGCTGTACTTTTGTCAAGGTGGATGTGACGGGCGCGTACACACCATCCCCCA	2220
Db	1081	GCCTCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTTGGCGCTCGGAGGCTCGTGGA	1140	Qy	2221	GGACAGGCTCACGAGGTCTATCGCCAGCATCATAAACCCAGAACACGTACTGCGTGG	2280
Qy	1141	GACCATCTTCTGGGTTCAGGCCCTGGATGCGCAGGACTTCCCGCGAGGTTGCCCGCCT	1200	Db	2221	GGACAGGCTCACGAGGTCTATCGCCAGCATCATAAACCCAGAACACGTACTGCGTGG	2280
Db	1141	GACCATCTTCTGGGTTCAGGCCCTGGATGCGCAGGACTTCCCGCGAGGTTGCCCGCCT	1200	Qy	2281	TCGGTATGCCGTGTCAGAAAGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA	2340
Qy	1201	GC CCGCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAACACGCGCA	1260	Db	2281	TCGGTATGCCGTGTCAGAAAGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA	2340
Db	1201	GC CCGCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAACACGCGCA	1260	Qy	2341	CGTCTCTACCTTGACACACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
Qy	1261	GTCC CCGCTACGGGGTGCTCTCTAAGAGCGCACTGCCCGCTCGGAGCTGCGGTCA CCGCAGC	1320	Db	2341	CGTCTCTACCTTGACACACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
Db	1261	GTCC CCGCTACGGGGTGCTCTCTAAGAGCGCACTGCCCGCTCGGAGCTGCGGTCA CCGCAGC	1320	Qy	2401	GACACGCCCTGAGGAGTCCGTCTCATTCGAGCAGAGCTCCTCTGAATGAGGCCAG	2460
Qy	1321	AGCCGGTGCTGTGCCGGGAGAACCCCAAGGCTCTGTGGCGGGCCCCCGAGGAGGGA	1380	Db	2401	GACACGCCCTGAGGAGTCCGTCTCATTCGAGCAGAGCTCCTCTGAATGAGGCCAG	2460
Db	1321	AGCCGGTGCTGTGCCGGGAGAACCCCAAGGCTCTGTGGCGGGCCCCCGAGGAGGGA	1380	Qy	2461	CAGTGGCTCTTCGAGCTCTTCCCTACGCTTCATGTCGACACCGCGCTGCGCATCAGGGG	2520
Qy	1381	CACAGACCCCGCTGCTGTGAGCTGCTGCCGACAGCAGCAGCAGCCTTGGCAGGTGTA	1440	Db	2461	CAGTGGCTCTTCGAGCTCTTCCCTACGCTTCATGTCGACACCGCGCTGCGCATCAGGGG	2520
Db	1381	CACAGACCCCGCTGCTGTGAGCTGCTGCCGACAGCAGCAGCAGCCTTGGCAGGTGTA	1440	Qy	2521	CAAGTCTTACCTGACGTGCGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTG	2580
Qy	1441	CGCTTCGTGCGGGCTGCTGCCGGGCTGTGTCGCCCGCTCTGGGCTCCAGGCA	1500	Db	2521	CAAGTCTTACCTGACGTGCGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTG	2580
Db	1441	CGCTTCGTGCGGGCTGCTGCCGGGCTGTGTCGCCCGCTCTGGGCTCCAGGCA	1500	Qy	2581	CAGCCTGTGTACGGCGACATGGAGAACAGCTGTTTGGCGGGATTCGGGGGACGGCT	2640
Qy	1501	CAACGACGGCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGATGCCAA	1560	Db	2581	CAGCCTGTGTACGGCGACATGGAGAACAGCTGTTTGGCGGGATTCGGGGGACGGCT	2640
Db	1501	CAACGACGGCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGATGCCAA	1560	Qy	2641	GTCTCTGCTGTTGGTGGATGATTTCTTGTGTTGGTACACCTCAGCTCACCACCGGAAAC	2700
Qy	1561	GCTCTCGCTCAGAGCTGACGTGGAAGATGACGCTGCGGACTGCGCTTGGCTGCGCAG	1620	Db	2641	GTCTCTGCTGTTGGTGGATGATTTCTTGTGTTGGTACACCTCAGCTCACCACCGGAAAC	2700
Db	1561	GCTCTCGCTCAGAGCTGACGTGGAAGATGACGCTGCGGACTGCGCTTGGCTGCGCAG	1620	Qy	2701	CTTCTCAGGACCTGCTGCGGAGTGTCCCTGAGTATGGCTGGGTGCTGAACTTGCAGAA	2760
Qy	1621	GAGCCAGAGGGTTGGCTGTTCGCCGCCGACAGCACCGCTCTCGGTGAGGAGATCCTGGC	1680	Db	2701	CTTCTCAGGACCTGCTGCGGAGTGTCCCTGAGTATGGCTGGGTGCTGAACTTGCAGAA	2760
Db	1621	GAGCCAGAGGGTTGGCTGTTCGCCGCCGACAGCACCGCTCTCGGTGAGGAGATCCTGGC	1680	Qy	2761	GACAGTGGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Qy	1681	CAAGTTCTGCTGCTGATGAGTGTGACGTGCTGCGAGCTGCTCAGGTCTTCTTTTAA	1740	Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Db	1681	CAAGTTCTGCTGCTGATGAGTGTGACGTGCTGCGAGCTGCTCAGGTCTTCTTTTAA	1740	Qy	2821	GCGGGCCACGGCTATTCCCTGGTGGCGCTGCTGCTGATACCGGACCTTGGAGGT	2880
Qy	1741	TGTCAGGAGACACAGCTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGTGGAG	1800	Db	2821	GCGGGCCACGGCTATTCCCTGGTGGCGCTGCTGCTGATACCGGACCTTGGAGGT	2880
Db	1741	TGTCAGGAGACACAGCTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGTGGAG	1800	Qy	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCCTTCAACCG	2940
Qy	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCATTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1860	Db	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCCTTCAACCG	2940
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCATTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1860	Qy	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCCGAAACTCTTTGGGGTCTTGGGGTGAAGTG	3000
Qy	1861	GGAAGCAGAGGTGAGGAGCATCGGAGCCAGCCAGCCGCTGCTGACGTCCAGACTCCG	1920	Db	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCCGAAACTCTTTGGGGTCTTGGGGTGAAGTG	3000
Db	1861	GGAAGCAGAGGTGAGGAGCATCGGAGCCAGCCAGCCGCTGCTGACGTCCAGACTCCG	1920	Qy	3001	TCACAGCTCTTCTGGATTTGAGGTGAACAGGCTCCACAGGCTGTCACACACATCTA	3060
Qy	1921	CTTCATCCCCAAGCCTGACGGGCTGCGCGGATTTGTGAACATGACTACGTCTCTGGAGC	1980	Db	3001	TCACAGCTCTTCTGGATTTGAGGTGAACAGGCTCCACAGGCTGTCACACACATCTA	3060
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGCGGATTTGTGAACATGACTACGTCTCTGGAGC	1980	Qy	3061	CAAGATCCTCTGCTGAGGCGGTACAGGTTTACGGCATGTGCTGACAGCTCCCATTTCA	3120
Qy	1981	CAGAAGCTTCCGAGAGAAAGAGGCGGCTCTCACCTCAGGGGTGAAGCAGCTGT	2040	Db	3061	CAAGATCCTCTGCTGAGGCGGTACAGGTTTACGGCATGTGCTGACAGCTCCCATTTCA	3120
Db	1981	CAGAAGCTTCCGAGAGAAAGAGGCGGCTCTCACCTCAGGGGTGAAGCAGCTGT	2040				

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QY 3121 TCAGAGAGTTGGAGAACCCACATTTTCTCGGGGTATCTCTGACAGGGCTCCCT 3180
Db 3121 TCAGAGAGTTGGAGAACCCACATTTTCTCGGGGTATCTCTGACAGGGCTCCCT 3180
QY 3181 CTGCTACTCCATCTCTGAAGCCAGAGAGGAGATGCTGGGGCCAGAGGGCGCG 3240
Db 3181 CTGCTACTCCATCTCTGAAGCCAGAGAGGAGATGCTGGGGCCAGAGGGCGCG 3240
QY 3241 CGGCGCTCTGCGCTCCGAGGCGTGCAGTGCTGCGCACCAAGCATTCCTGCTCAAGCT 3300
Db 3241 CGGCGCTCTGCGCTCCGAGGCGTGCAGTGCTGCGCACCAAGCATTCCTGCTCAAGCT 3300
QY 3301 GACTCGACACCGTGTCACTAGTGCACCTCTCTGGGTCACTCAGGACAGCCAGAGCCA 3360
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QY 3361 GCTGAGTCGGAAGCTCCCGGGGAGACGCTGACTGCTGAGGCGCGAGCAACCCGGC 3420
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QY 3961 GAGGTGCTGTGGAGTAAATACTGAATATATAGTATTTTTCAGTTTGTAAAAAAA 4015
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RESULT 4

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PCT-US02-33146-19
; Sequence 19, Application PC/TUS0233146
; GENERAL INFORMATION:
; APPLICANT: University of Rochester Medical Center
; APPLICANT: Rowley, Peter
; TITLE OF INVENTION: Telomerase Interference
; FILE REFERENCE: FP-71506-2/RET/SRN
; CURRENT APPLICATION NUMBER: PCT/US02/33146
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 19
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-33146-19

Query Match      100.0%; Score 4015; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 60
QY 61 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 120
Db 61 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 120
QY 121 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 180
Db 121 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 180
QY 181 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 240
Db 181 GCAGCGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 240
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Db 301 CCGAGTGGCTCTGCTGCGACGTGGGAAGCCCTGCGCCCGCCGACACCCCGGAGTCC 360
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Db 361 GCTGCTGGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 CCTGCGCAACAGTGTACAGGCTGTGCGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGG 480
Db 421 CCTGCGCAACAGTGTACAGGCTGTGCGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGG 480
QY 481 CCGCGTGGCGGCGACGACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 CCGCGTGGCGGCGACGACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GGCTCCAGCTGTGCGCTTACCAGGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 541 GGCTCCAGCTGTGCGCTTACCAGGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 601 TCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 601 TCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 CTGGAACCATAGCTGTAGGAGGCGCGGGTCCCTGCGGGCTGCGACCGCGGGTGGCGAG 720
Db 661 CTGGAACCATAGCTGTAGGAGGCGCGGGTCCCTGCGGGCTGCGACCGCGGGTGGCGAG 720
QY 721 GAGCGCGGGGCGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAG 780
Db 721 GAGCGCGGGGCGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAG 780
QY 781 TGCCCTGTAGCGCGGAGGAGCGCGCGTGGGCGAGGGTCTTGGCGGCGACCGCGGCGAG 840
Db 781 TGCCCTGTAGCGCGGAGGAGCGCGCGTGGGCGAGGGTCTTGGCGGCGACCGCGGCGAG 840
QY 841 GCGTGGACCGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAG 900
Db 841 GCGTGGACCGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAG 900
QY 901 CACCTCTTTGGAGGCTGCGCTCTTGGCAGCGCGGCTCTTGGCAGCGGCTCTTGGCAGCG 960
Db 901 CACCTCTTTGGAGGCTGCGCTCTTGGCAGCGCGGCTCTTGGCAGCGGCTCTTGGCAGCG 960
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Qy	961	GCACAGCGGGCCCCCCTCCACATCGCGGCCACACAGTCCCTGGGACACGCTTGTCC	1020
Db	961	GCACACGCGGGCCCCCCTCCACATCGCGGGCCACACGTCCTCTGGGACACGCTTGTCC	1020
Qy	1021	CCCGGTGTACGCGGACCAAGCACATCTCTACTCTCAGGCGCAAGGACGAGTGG	1080
Db	1021	CCCGGTGTACGCGGACCAAGCACATCTCTACTCTCAGGCGCAAGGACGAGTGG	1080
Qy	1081	GCCTCTCTTCTACTCAGCTCTGTAGGCGCCAGCTGTACTGGCGCTCGGAGGCTCGTGA	1140
Db	1081	GCCTCTCTTCTACTCAGCTCTGTAGGCGCCAGCTGTACTGGCGCTCGGAGGCTCGTGA	1140
Qy	1141	GACCATCTTCTGGGTTTCAGGCCCTTGATGCGAGGACTCCCCGAGTTGGCCGCGCT	1200
Db	1141	GACCATCTTCTGGGTTTCAGGCCCTTGATGCGAGGACTCCCCGAGTTGGCCGCGCT	1200
Qy	1201	GCCCCAGCGCTACTGTGCAATGCGGCCCTGTCTTCTTGGAGCTGTCTTGGAAACACACGCA	1260
Db	1201	GCCCCAGCGCTACTGTGCAATGCGGCCCTGTCTTCTTGGAGCTGTCTTGGAAACACACGCA	1260
Qy	1261	GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTTCGAGCTTCGCTCACCCAGC	1320
Db	1261	GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTTCGAGCTTCGCTCACCCAGC	1320
Qy	1321	AGCGGTGTCTGTGCCGGGAGAAAGCCCCAGGGCTCTGTGGGGCCCCCGAGGAGGA	1380
Db	1321	AGCGGTGTCTGTGCCGGGAGAAAGCCCCAGGGCTCTGTGGGGCCCCCGAGGAGGA	1380
Qy	1381	CACAGACCCCGTGCCTGGTGCAGCTGTCTCCGCCAGCACAGCAGCCCTGGCAGGTGA	1440
Db	1381	CACAGACCCCGTGCCTGGTGCAGCTGTCTCCGCCAGCACAGCAGCCCTGGCAGGTGA	1440
Qy	1441	CGGTCGTGCGGGCTGTGTCGCCGGTGTGTGCCCCAGGGCTCTGGGGTTCACAGCA	1500
Db	1441	CGGTCGTGCGGGCTGTGTCGCCGGTGTGTGCCCCAGGGCTCTGGGGTTCACAGCA	1500
Qy	1501	CAACGAACCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTCGGGAAGCATGCCAA	1560
Db	1501	CAACGAACCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTCGGGAAGCATGCCAA	1560
Qy	1561	GCTCTCGCTCAGGAGTGCAGTGGGAAGATGACGTCGCGGACTTGGCTGGCTGGCAG	1620
Db	1561	GCTCTCGCTCAGGAGTGCAGTGGGAAGATGACGTCGCGGACTTGGCTGGCTGGCAG	1620
Qy	1621	GAGCCAGGGTTGGTGTGTTCCGCGCCGACAGCACCGTCTGCGTGAGGAGATCTGGC	1680
Db	1621	GAGCCAGGGTTGGTGTGTTCCGCGCGCAGACACCGTCTGCGTGAGGAGATCTGGC	1680
Qy	1681	CAAGTCTCTCACTGGCTGATGATGTGTACGTCTGCGAGCTCTCAGTCTTCTTTTA	1740
Db	1681	CAAGTCTCTCACTGGCTGATGATGTGTACGTCTGCGAGCTGCTCAGTCTTCTTTTA	1740
Qy	1741	TGTACGGAGACCACTTTCAAAGAACAAGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
Db	1741	TGTACGGAGACCACTTTCAAAGAACAAGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
Qy	1801	CAAGTTCGAAGCATTTGAATTCAGACGACTTGAAGAGGGTGACGTGGGAGCTGTC	1860
Db	1801	CAAGTTCGAAGCATTTGAATTCAGACGACTTGAAGAGGGTGACGTGGGAGCTGTC	1860
Qy	1861	GGAAGCAGAGTTCAGGCAGCATCGGAAGCCAGGCCCGCTCTGACGTCCAGACTCCG	1920
Db	1861	GGAAGCAGAGTTCAGGCAGCATCGGAAGCCAGGCCCGCTCTGACGTCCAGACTCCG	1920
Qy	1921	CTTCATCCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGGACTACGTCTGGGAGC	1980
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGGACTACGTCTGGGAGC	1980
Qy	1981	CAGACGTTCCGAGAGAAAGAGGCCGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040
Db	1981	CAGACGTTCCGAGAGAAAGAGGCCGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040

QY	2041	CAGGCTGCTCAACTACAGGGGGCGCGCGCCCGGGCCTCCTGTGGCGCCCTCTGTGTGGG	2100
DB	2041	CAGGCTGCTCAACTACAGGGGGCGCGCGCCCGGGCCTCCTGTGGCGCCCTCTGTGTGGG	2100
QY	2101	CCTGGACGATACACAGGCGCTTGGCGACCTTCCTGTGCTGCTGCTGGCGCCAGACCC	2160
DB	2101	CCTGGACGATATCCACAGGCGCTTGGCGACCTTCCTGTGCTGCTGCTGGCGCCAGACCC	2160
QY	2161	GCCGCTTGAGTGTACTTTTCAAGGTGGATGTGACGGGCGGTACGACACCATCCGCCA	2220
DB	2161	GCCGCTTGAGTGTACTTTTCAAGGTGGATGTGACGGGCGGTACGACACCATCCGCCA	2220
QY	2221	GGACAGGCTCACGGAGTCAATCGCCACGATCATCAAAACCCAGACGCTTCACAGACCA	2280
DB	2221	GGACAGGCTCACGGAGTCAATCGCCACGATCATCAAAACCCAGACGCTTCACAGACCA	2280
QY	2281	TCGGTATCCGCTGCTCAGAGGCGCCCATGGGACGTCGCGAAGGCTTCACAGGCGCA	2340
DB	2281	TCGGTATCCGCTGCTCAGAGGCGCCCATGGGACGTCGCGAAGGCTTCACAGGCGCA	2340
QY	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATCGACAGTTCTGTGCTCACCTGCAGGA	2400
DB	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATCGACAGTTCTGTGCTCACCTGCAGGA	2400
QY	2401	GACAGCCCGTGAAGGATCCGCTGCTATCGAGCAGAGTCTCTCCTGAATGAGGCCAG	2460
DB	2401	GACAGCCCGTGAAGGATCCGCTGCTATCGAGCAGAGTCTCTCCTGAATGAGGCCAG	2460
QY	2461	CAGTGGCTCTTCCACGCTTCTCCACGCTTCATGTCGCCACACGCGCTGCGCATCAGGG	2520
DB	2461	CAGTGGCTCTTCCACGCTTCTCCACGCTTCATGTCGCCACACGCGCTGCGCATCAGGG	2520
QY	2521	CAAGTCTTACGTCAGGCGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
DB	2521	CAAGTCTTACGTCAGGCGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
QY	2581	CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
DB	2581	CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
QY	2641	GCTCCTGCTTGTGTGATGATTCTTGTGTCACACCTCACCTCACCCACCGGCAAC	2700
DB	2641	GCTCCTGCTTGTGTGATGATTCTTGTGTCACACCTCACCTCACCCACCGGCAAC	2700
QY	2701	CTTCCTCAGGACCTTGCTCCAGGTGCTCCCTGAGTATGGCTGCTGCTGAACTTGCAGAA	2760
DB	2701	CTTCCTCAGGACCTTGCTCCAGGTGCTCCCTGAGTATGGCTGCTGCTGAACTTGCAGAA	2760
QY	2761	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCGCTTGGTGGCACGGCTTTTGTTCAGAT	2820
DB	2761	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCGCTTGGTGGCACGGCTTTTGTTCAGAT	2820
QY	2821	GCCGGCCACGGCTATTCCTGCTGGGCGCTGCTGCTGGATACCGGACCTTGAGGT	2880
DB	2821	GCCGGCCACGGCTATTCCTGCTGGGCGCTGCTGCTGGATACCGGACCTTGAGGT	2880
QY	2881	GCAGAGGACTTACTCCAGCTATGCCCAGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
DB	2881	GCAGAGGACTTACTCCAGCTATGCCCAGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGGAGAACATGCGTTCGCAAACTCTTTGGGCTCTTGGGCTGAAATG	3000
DB	2941	CGGCTTCAAGGCTGGGAGAACATGCGTTCGCAAACTCTTTGGGCTCTTGGGCTGAAATG	3000
QY	3001	TCACAGCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3060
DB	3001	TCACAGCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3060
QY	3061	CAAGATCTCCTGCTGCAGGCGTACAGGTTTTCAGCGATGTGCTGCAGCTGCCATTTTCA	3120
DB	3061	CAAGATCTCCTGCTGCAGGCGTACAGGTTTTCAGCGATGTGCTGCAGCTGCCATTTTCA	3120
QY	3121	TCAGCAGTTTTGGAAGAACCCACATTTTTTCTCGGCTCATCTCTGACACGGCTCCCT	3180

Db	661	CTGGAACCATAGGTGAGGAGCGCGGGGTCCCTTGGGCTGCCAGCCCCGGGTGGAG	720
Qy	721	GAGCGCGGGGAGTGCACAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGGGTGGCG	780
Db	721	GAGCGCGGGGAGTGCACAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGGGTGGCG	780
Qy	781	TGCCCCGTGAGCCGAGCGGAGCGCCGTTGGGCAAGGGTCTGGGCCACCCGGGAGGAC	840
Db	781	TGCCCCGTGAGCCGAGCGGAGCGCCGTTGGGCAAGGGTCTGGGCCACCCGGGAGGAC	840
Qy	841	GCSTGGACCAAGTACCGTGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
Db	841	GCSTGGACCAAGTACCGTGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
Qy	901	CACCTCTTTTGGAGGGTGCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
Db	901	CACCTCTTTTGGAGGGTGCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
Qy	961	GCACCAAGCGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACAGCCTGTGC	1020
Db	961	GCACCAAGCGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACAGCCTGTGC	1020
Qy	1021	CCGGGTGTACCGGAGACCAAGCACTTCTCTACTCTCAGCGCCACTCCACCCCATCCGTGGGCGGCCA	1080
Db	1021	CCGGGTGTACCGGAGACCAAGCACTTCTCTACTCTCAGCGCCACTCCACCCCATCCGTGGGCGGCCA	1080
Qy	1081	GCCTCTCTTCTACTCAGCTCTCTGAGGCCAGCCCTGACTGTGGGCTGCGAGGCTCGTGA	1140
Db	1081	GCCTCTCTTCTACTCAGCTCTCTGAGGCCAGCCCTGACTGTGGGCTGCGAGGCTCGTGA	1140
Qy	1141	GACCATCTTTCTGGGTTCAGGGCCCTGGATGCCAGGACTCCCGCGAGGTTGCCCGCCT	1200
Db	1141	GACCATCTTTCTGGGTTCAGGGCCCTGGATGCCAGGACTCCCGCGAGGTTGCCCGCCT	1200
Qy	1201	GCCCCAGCGTACTTGGCAATCGGCCCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGT	1260
Db	1201	GCCCCAGCGTACTTGGCAATCGGCCCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGT	1260
Qy	1261	GTGCCCCCTACGGGGTGTCTCTAAGAGCGACTGCCCGCTCGAGCTGCGGCTCAGGAGGA	1320
Db	1261	GTGCCCCCTACGGGGTGTCTCTAAGAGCGACTGCCCGCTCGAGCTGCGGCTCAGGAGGA	1320
Qy	1321	AGCGGTGTCTGTGCCGGAGAGCCCGAGGCTCTGTGGCGGCCCGCCAGGAGGAGGA	1380
Db	1321	AGCGGTGTCTGTGCCGGAGAGCCCGAGGCTCTGTGGCGGCCCGCCAGGAGGAGGA	1380
Qy	1381	CACAGACCCCGTCTGT	1440
Db	1381	CACAGACCCCGTCTGT	1440
Qy	1441	CGGTTGT	1500
Db	1441	CGGTTGT	1500
Qy	1501	CAAGACCCCGTCTCTCAGGACACCAAGAGTGTATCTCCCTGGGGAAGCATGCCAA	1560
Db	1501	CAAGACCCCGTCTCTCAGGACACCAAGAGTGTATCTCCCTGGGGAAGCATGCCAA	1560
Qy	1561	GCTCTGT	1620
Db	1561	GCTCTGT	1620
Qy	1621	GAGCCCAAGGGT	1680
Db	1621	GAGCCCAAGGGT	1680
Qy	1681	CAGTTCCTGCATGGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1740
Db	1681	CAGTTCCTGCATGGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1740
Qy	1741	TGTCACGAGACCAAGCTTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTGTGAG	1800
Db	1741	TGTCACGAGACCAAGCTTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTGTGAG	1800
Qy	1801	CAAGTTTCAAAGCATTTGAATCAGACAGCACTTTGAAGAGGTTGACGTGCGGAGCTGTC	1860
Db	1801	CAAGTTTCAAAGCATTTGAATCAGACAGCACTTTGAAGAGGTTGACGTGCGGAGCTGTC	1860
Qy	1861	GGAGCAGAGGTCAGGAGCATCGGNAAGCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Db	1861	GGAGCAGAGGTCAGGAGCATCGGNAAGCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Qy	1921	CTTTCATCCCCAAGCTGACGGGTGCGGCCGATTTGAACATGACGTACGTGCTGCGGAGC	1980
Db	1921	CTTTCATCCCCAAGCTGACGGGTGCGGCCGATTTGAACATGACGTACGTGCTGCGGAGC	1980
Qy	1981	CAGAACGTTCCGAGAGAAAGAGGCCGCGCTCTACCTCAGAGGTTGAAGCACTGTT	2040
Db	1981	CAGAACGTTCCGAGAGAAAGAGGCCGCGCTCTACCTCAGAGGTTGAAGCACTGTT	2040
Qy	2041	CAGCGTCTCAACTACGAGCGGCGGCCCGCCGCTCTTGGGCGCTCTGTGTGTGG	2100
Db	2041	CAGCGTCTCAACTACGAGCGGCGGCCCGCCGCTCTTGGGCGCTCTGTGTGTGG	2100
Qy	2101	CTTGGAGCATATCACAGGCGCTGGCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	2160
Db	2101	CTTGGAGCATATCACAGGCGCTGGCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	2160
Qy	2161	GCCTCTGAGCTGTACTTTTCAAGGTGGATGTGACGGGCGCTTACACACCACTCCGCCA	2220
Db	2161	GCCTCTGAGCTGTACTTTTCAAGGTGGATGTGACGGGCGCTTACACACCACTCCGCCA	2220
Qy	2221	GGACAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAACAGTACTGCTGCG	2280
Db	2221	GGACAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAACAGTACTGCTGCG	2280
Qy	2281	TCGGTATCGGCTGTCAGAGCGCCCGCATGCGCAGCATCATCAAAACCCAGAACAGGCA	2340
Db	2281	TCGGTATCGGCTGTCAGAGCGCCCGCATGCGCAGCATCATCAAAACCCAGAACAGGCA	2340
Qy	2341	CGTCTCTACCTTGACAGACCTCCAGCGCTACATCGACAGTTCGTGCTCACCCTGACGA	2400
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCGCTACATCGACAGTTCGTGCTCACCCTGACGA	2400
Qy	2401	GACGACCCCGCTGAGGATGCCCTGTCATCGAGCAGAGCTCCTCCCTGATGAGGCGAG	2460
Db	2401	GACGACCCCGCTGAGGATGCCCTGTCATCGAGCAGAGCTCCTCCCTGATGAGGCGAG	2460
Qy	2461	CAGTGGGCTCTTGCAGCTCTTCTACCTTACCTGTCACACCGCTGCGCATCAGGGG	2520
Db	2461	CAGTGGGCTCTTGCAGCTCTTCTACCTTACCTGTCACACCGCTGCGCATCAGGGG	2520
Qy	2521	CAAGTCTACGTCCAGTCCAGGGGATCCCGAGGGTCCATCCTCTCCACGCTGCTGTG	2580
Db	2521	CAAGTCTACGTCCAGTCCAGGGGATCCCGAGGGTCCATCCTCTCCACGCTGCTGTG	2580
Qy	2581	CAGCCTGTGTACGGCAGCATGAGAACAGTGTGCGGGGATTCGGGGGAGCGGCT	2640
Db	2581	CAGCCTGTGTACGGCAGCATGAGAACAGTGTGCGGGGATTCGGGGGAGCGGCT	2640
Qy	2641	GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2700
Db	2641	GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2700
Qy	2701	CTTCTCTCAGGACCTTGTCTCGAGGTGTCCTTGAGTATGGCTGCTGCTGCTGCTGCTG	2760
Db	2701	CTTCTCTCAGGACCTTGTCTCGAGGTGTCCTTGAGTATGGCTGCTGCTGCTGCTGCTG	2760
Qy	2761	GACAGTGTGAACTTCTCCTGTAGAGAGAGGCGCTGGGTGGGACAGCGCTTTTGTTCAG	2820
Db	2761	GACAGTGTGAACTTCTCCTGTAGAGAGAGGCGCTGGGTGGGACAGCGCTTTTGTTCAG	2820
Qy	2821	GCGGCCACGCGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
Db	2821	GCGGCCACGCGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880

QY	3961	GAGTCTCTGGGAGTAAAAACTGAATATACAGTTTTCAGCTTTTGAAAAAA	4015
Db	3961	GAGTCTGTGGGAGTAAAAACTGAATATACAGTTTTCAGCTTTTGAAAAAA	4015
 RESULT 6 PCT-US99-07097-1 ; Sequence 1, Application PC/TUS9907097 ; GENERAL INFORMATION: ; APPLICANT: Morin, Gregg B. ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants ; FILE REFERENCE: 015389-003310PC ; CURRENT APPLICATION NUMBER: PCT/US99/07097 ; CURRENT FILING DATE: 1999-03-31 ; EARLIER APPLICATION NUMBER: US 09/052,864 ; EARLIER FILING DATE: 1998-03-31 ; EARLIER APPLICATION NUMBER: US 09/128,354 ; EARLIER FILING DATE: 1998-08-03 ; NUMBER OF SEQ ID NOS: 21 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 4015 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (56)..(3454) ; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) CDNA PCT-US99-07097-1			
 Query Match 100.0%; Score 4015; DB 1; Length 4015; Best Local Similarity 100.0%; Pred. No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps			
QY	1	GCACCGCTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCGCCACCACCCCGCGATGCC	
Db	1	GCACCGCTGGGCTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGCCACCACCCCGCGATGCC	
QY	61	GCGGCGCTCCCCTCCGCGAGCCGTGCGCTCCCTCTGCTGCGCAGCCACCTACCGCGCAGGTGCT	
Db	61	GCGGCGCTCCCCTCCGCGAGCCGTGCGCTCCCTCTGCTGCGCAGCCACCTACCGCGCAGGTGCT	
QY	121	GCCGCTGGCCACAGTTCTGTGGCGGCCCTTGGGGCCCCCAGGGCTTGGCGGCTGTGCAGCCGCG	
Db	121	GCCGCTGGCCACAGTTCTGTGGCGGCCCTTGGGGCCCCCAGGGCTTGGCGGCTGTGCAGCCGCG	
QY	181	GGACCCGGCGGCTTTCCGCGCGCTGTGTGGCCACGTGCTGGTGTGCTGCCCTGGGACGCG	
Db	181	GGACCCGGCGGCTTTCCGCGCGCTGTGTGGCCACGTGCTGGTGTGCTGCCCTGGGACGCG	
QY	241	ACGGCGCGCCCCCCCCCGCGGCCCTCTCTTCCGCGCAGGTGCTGTCAAGAGCTGTGTGGG	
Db	241	ACGGCGCGCCCCCCCCCGCGGCCCTCTCTTCCGCGCAGGTGCTGTCAAGAGCTGTGTGGG	
QY	301	CCGAGTGTGCAGAGGCTGTCCGAGCGCGCGGCCCGAAGACGTGCTGGCTTCGGCTTCG	
Db	301	CCGAGTGTGTGAGAGGCTGTCCGAGCGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCG	
QY	361	GCTGCTGGACGGGCGCCCGCGGGGCGCCCCCGCGAGGCTTACACACAGCGTGCAGCT	
Db	361	GCTGCTGGACGGGCGCCCGCGGGGCGCCCCCGCGAGGCTTACACACAGCGTGCAGCT	
QY	421	CCTGCCCAACACGCTGACCGACGACCTGCGGGGAGCGGGGCGTGTGCGTGTGCTGCG	
Db	421	CCTGCCCAACACGCTGACCGACGACCTGCGGGGAGCGGGGCGTGTGCGTGTGCTGCG	
QY	481	CCGGTGGGGCAGCAGCTGCTGGTTACCTGCTGCAGCTGCGCGCTCTTTGCTGGTGG	
Db	481	CCGGTGGGGCAGCAGCTGCTGGTTACCTGCTGCAGCTGCGCGCTCTTTGCTGGTGG	
QY	541	GGCTCCCAAGCTCGCCCTACACAGGTGTGGGGGCCCGCGCTGTACACAGCTCGGCGCTGCCACA	

Db 541 GGCTCCAGCTGGCCCTACCAAGGTGTGGGGCCGCCGTGTACCAAGCTGGCGCCTGCCAC 600
QY 601 TCAGGCCCCGGCCCCCACCACAGCTAGTGGACCCCGAAGCCGCTTGGGATGCGAAGCGGC 660
Db 601 TCAGGCCCCGGCCCCCACCACAGCTAGTGGACCCCGAAGCCGCTTGGGATGCGAAGCGGC 660
QY 661 CTGGAAACCATAGGCTCAGGAGGCGCGGGGTCCCTTGGGCTGCCAGCCCCGGGTGCGAG 720
Db 661 CTGGAAACCATAGGCTCAGGAGGCGCGGGGTCCCTTGGGCTGCCAGCCCCGGGTGCGAG 720
QY 721 GAGGCGGGGGGAGTGCACAGCGAAAGTCTGCCGTTGCCAAGAGGCCAGGGCGTGGCG 780
Db 721 GAGGCGGGGGGAGTGCACAGCGAAGTCTGCCGTTGCCAAGAGGCCAGGGCGTGGCG 780
QY 781 TGCCCCGTAGCCGAGCGGACGCCCTTGGGAGGGGTCTTGGGCGCCACCCGGGCGAGGAC 840
Db 781 TGCCCCGTAGCCGAGCGGACGCCCTTGGGAGGGGTCTTGGGCGCCACCCGGGCGAGGAC 840
QY 841 GCGTGACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACCGCCGCAAGAGC 900
Db 841 GCGTGACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACCGCCGCAAGAGC 900
QY 901 CACCTCTTTGGAGGGTGCCTCTCTGGCACGGCCACTCCCAACCCATCCGTGGCGCGCCA 960
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QY 961 GCACACGGGGGCCCCCACCATCCACATCGCGGGCCACACGCTCCCTGGGACAGCGCTTGTC 1020
Db 961 GCACACGGGGGCCCCCACCATCCACATCGCGGGCCACACGCTCCCTGGGACAGCGCTTGTC 1020
QY 1021 CCGGTGTACGGGAGACCAACGACTTCTCTACTCTCAGGCGCAAGAGGAGCAGTGG 1080
Db 1021 CCGGTGTACGGGAGACCAACGACTTCTCTACTCTCAGGCGCAAGAGGAGCAGTGG 1080
QY 1081 GCGCTCTTCTACTCTCAGTCTCTGAGGCCACGCTTCTGAGGCTCGGAGGCTCGTGGA 1140
Db 1081 GCGCTCTTCTACTCTCAGTCTCTGAGGCCACGCTTCTGAGGCTCGGAGGCTCGTGGA 1140
QY 1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCGCAGGACTTCCCGCAGGTTGCCCGCCT 1200
Db 1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCGCAGGACTTCCCGCAGGTTGCCCGCCT 1200
QY 1201 GCGCCAGCGCTACTGCGCAATCGGCCCTGTTCTGAGAGCTGCTTGGAGCTTGGNAACCGCGCA 1260
Db 1201 GCGCCAGCGCTACTGCGCAATCGGCCCTGTTCTGAGAGCTGCTTGGAGCTTGGNAACCGCGCA 1260
QY 1261 GTGCCCTTACGGGGTCTCCTCAAGACGCACCTGCCCGCTCGAGCTGCGGCTCACCCAGC 1320
Db 1261 GTGCCCTTACGGGGTCTCCTCAAGACGCACCTGCCCGCTCGAGCTGCGGCTCACCCAGC 1320
QY 1321 AGCCGCTGTGTGCCCCGGAGAACGCCAGAGGCTCTGTGGCGGCCCGCAGGAGGAGGA 1380
Db 1321 AGCCGCTGTGTGCCCCGGAGAACGCCAGAGGCTCTGTGGCGGCCCGCAGGAGGAGGA 1380
QY 1381 CACAGACCCCGCTGCTGTGTCAGCTGTCTCCGACGACAGCAGCCCCCTGGCAGGTGTA 1440
Db 1381 CACAGACCCCGCTGCTGTGTCAGCTGTCTCCGACGACAGCAGCCCCCTGGCAGGTGTA 1440
QY 1441 CGGCTTCTGTGCGGGCTGTGCTGCGCGGCTGTGTGCCCGCCAGGCGCTTGGGGCTCCAGGCA 1500
Db 1441 CGGCTTCTGTGCGGGCTGTGCTGCGCGGCTGTGTGCCCGCCAGGCGCTTGGGGCTCCAGGCA 1500
QY 1501 CAACGAACCGCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAA 1560
Db 1501 CAACGAACCGCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAA 1560
QY 1561 GCTCTCGCTGCAGGAGCTGACGTGGAGATGACGCTGCGGGACTGCGCTTGGCTGGCGAG 1620
Db 1561 GCTCTCGCTGCAGGAGCTGACGTGGAGATGACGCTGCGGGACTGCGCTTGGCTGGCGAG 1620
QY 1621 GAGCCAGGGGTTGGCTGTCTTCCGGCCGACAGCACCGCTCTCGCTGAGGAGATCCTGGC 1680
Db 1621 GAGCCAGGGGTTGGCTGTCTTCCGGCCGACAGCACCGCTCTCGCTGAGGAGATCCTGGC 1680

QY 1681 CAAAGTTCTGCACTGCGTGAATGAGTGTGTACGTGCTGAGCTGCTCAGGTCCTTCTTTTA 1740
Db 1681 CAAAGTTCTGCACTGCGTGAATGAGTGTGTACGTGCTGAGCTGCTCAGGTCCTTCTTTTA 1740
QY 1741 TGTACGGAGACCACTTTTCAAAGAACAGGCTCTTTTCTACGGNAGAGTGTCTGGAG 1800
Db 1741 TGTACGGAGACCACTTTTCAAAGAACAGGCTCTTTTCTACGGNAGAGTGTCTGGAG 1800
QY 1801 CAAAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGCTGACGCTCGGGAGCTGTC 1860
Db 1801 CAAAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGCTGACGCTCGGGAGCTGTC 1860
QY 1861 GGAAGCAGAGGTCAGGAGCATCGGGAAGCAGGCCGCCCTCTGCTGACGTCACAGCTCCG 1920
Db 1861 GGAAGCAGAGGTCAGGAGCATCGGGAAGCAGGCCGCCCTCTGCTGACGTCACAGCTCCG 1920
QY 1921 CTTTATCCCAAGCCTGACGGGCTGGCGCGATTTGAAACATGGACTTACGCTGGGAGC 1980
Db 1921 CTTTATCCCAAGCCTGACGGGCTGGCGCGATTTGAAACATGGACTTACGCTGGGAGC 1980
QY 1981 CAGAAGCTTCCCGCAGAGAAAGAGGCGCGCTCTCACCTCGAGGGTGAAGCAGCTGTT 2040
Db 1981 CAGAAGCTTCCCGCAGAGAAAGAGGCGCGCTCTCACCTCGAGGGTGAAGCAGCTGTT 2040
QY 2041 CAGCGTGTCAACTACAGGCGGGCGGCCCTCTTGGGCGCTCTGTGTGGG 2100
Db 2041 CAGCGTGTCAACTACAGGCGGGCGGCCCTCTTGGGCGCTCTGTGTGGG 2100
QY 2101 CTTGGAGCATATCCAGGGCTTGGCGCACCTTCTGCTGCTGCTGGGGCCACGAGCC 2160
Db 2101 CTTGGAGCATATCCAGGGCTTGGCGCACCTTCTGCTGCTGCTGGGGCCACGAGCC 2160
QY 2161 GCGCCTGAGCTGACTTTGTCAAGGTGGATGTGAGCGGCGGTACACACCATCCCCCA 2220
Db 2161 GCGCCTGAGCTGACTTTGTCAAGGTGGATGTGAGCGGCGGTACGACACCATCCCCCA 2220
QY 2221 GGAAGGCTCACGAGGTCATGCCAGCATCATCAAACCCAGAACACGTCGCTGCG 2280
Db 2221 GGAAGGCTCACGAGGTCATGCCAGCATCATCAAACCCAGAACACGTCGCTGCG 2280
QY 2281 TCGGTATGCGGTGGTCAGAAAGCGGCCCATGAGGCTCGGCAAGGCTTCAAGAGCCA 2340
Db 2281 TCGGTATGCGGTGGTCAGAAAGCGGCCCATGAGGCTCGGCAAGGCTTCAAGAGCCA 2340
QY 2341 CGTCTTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCA 2400
Db 2341 CGTCTTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCA 2400
QY 2401 GACCAAGCGCTGAGGATGCCGTGTCATGAGCAGAGCTTCTTCCCTGAATGAGGCCAG 2460
Db 2401 GACCAAGCGCTGAGGATGCCGTGTCATGAGCAGAGCTTCTTCCCTGAATGAGGCCAG 2460
QY 2461 CAGTGGCTTCTGAGCTTCTTACGCTTCTGTCATGTCACCGCTGCGGATCGGCTGAGGG 2520
Db 2461 CAGTGGCTTCTGAGCTTCTTACGCTTCTGTCATGTCACCGCTGCGGATCGGCTGAGGG 2520
QY 2521 CAAAGTCTTACGCTGCGGAGTCCCGAGGCTTCCATCTCTCCACGCTGCTG 2580
Db 2521 CAAAGTCTTACGCTGCGGAGTCCCGAGGATCCCGAGGCTTCCATCTCTCCACGCTGCTG 2580
QY 2581 CAGCCTGTGTACGGGACATGAGAAAGCTGTTTGGGGGATTCGGCGGACGCGCT 2640
Db 2581 CAGCCTGTGTACGGGACATGAGAAAGCTGTTTGGGGGATTCGGCGGACGCGCT 2640
QY 2641 GCTCCTGCGTTTGGTGGATGATTTCTTGGTGGTACACCTTACCTCACCCACGCGAAGC 2700
Db 2641 GCTCCTGCGTTTGGTGGATGATTTCTTGGTGGTACACCTTACCTCACCCACGCGAAGC 2700
QY 2701 CTTTCTCAGGACCTGGTCCGAGGTGCTCCTGAGTATGGCTGGTGGTGAACCTTGGCGAA 2760
Db 2701 CTTTCTCAGGACCTGGTCCGAGGTGCTCCTGAGTATGGCTGGTGGTGAACCTTGGCGAA 2760

[illegible]

Query Match									
Best Local Similarity			100.0%; Score 4015; DB 2; Length 4015;						
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCAGCGTGGTCTCTGCTGCGCAGGTGGGAGGCCCTGGCCCGGCCACCCCGCGATGCC	60						
Db	1	GCAGCGTGGTCTCTGCTGCGCAGCTGGGAGGCCCTGGCCCGGCCACCCCGCGATGCC	60						
Qy	61	CGCGCTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACCTACCGCAGGTGCT	120						
Db	61	CGCGCTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACCTACCGCAGGTGCT	120						
Qy	121	CGCGCTGGCACGTTCTGGCGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTCAGCGCGG	180						
Db	121	CGCGCTGGCACGTTCTGGCGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTCAGCGCGG	180						
Qy	181	GGACCCGGCGCTTTCCGCGCGCTGGTGCGCCAGTGCTGCTGGCTGCGCTGGGACGC	240						
Db	181	GGACCCGGCGCTTTCCGCGCGCTGGTGCGCCAGTGCTGCTGGCTGCGCTGGGACGC	240						
Qy	241	ACGSCCGCCCCCGCCCTCTTCCGCGAGGTGCTGCTGAAGAGCTGTGTGGC	300						
Db	241	ACGSCCGCCCCCGCCCTCTTCCGCGAGGTGCTGCTGAAGAGCTGTGTGGC	300						
Qy	301	CCGAGTCTGAGAGGCTGTGCGAGCGCGCGGAGAACGTGCTGCGCTTCGCTTCGC	360						
Db	301	CCGAGTCTGAGAGGCTGTGCGAGCGCGCGGAGAACGTGCTGCGCTTCGCTTCGC	360						
Qy	361	GCTCTGAGCGGGCCCGCGGGGCCCCCGAGGCCCTTACCACACAGCTGGCAGCTA	420						
Db	361	GCTCTGAGCGGGCCCGCGGGGCCCCCGAGGCCCTTACCACACAGCTGGCAGCTA	420						
Qy	421	CCTGCCAACACAGGTGACCGACGACATGCGGGGAGCGGGCGCTGCTGCTGGC	480						
Db	421	CCTGCCAACACAGGTGACCGACGACATGCGGGGAGCGGGCGCTGCTGCTGGC	480						
Qy	481	CCGGCTGGGGACGACGTGCTGTTACCTGCTGGGACAGCTGCGCGCTCTTTGTGCTGGT	540						
Db	481	CCGGCTGGGGACGACGTGCTGTTACCTGCTGGGACAGCTGCGCGCTCTTTGTGCTGGT	540						
Qy	541	GGCTCCAGCTGCGCCCTACCAAGTGTGCGGGCGCGCTGTACCAGCTGCGCGCTGCCAC	600						
Db	541	GGCTCCAGCTGCGCCCTACCAAGTGTGCGGGCGCGCTGTACCAGCTGCGCGCTGCCAC	600						
Qy	601	TCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGCGCTGGGATGCCAACGGCG	660						
Db	601	TCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGCGCTGGGATGCCAACGGCG	660						
Qy	661	CTGGAACATAGCGTCAAGGAGCGCGGGTCCCGCTGGCGCTGCCACGCCCGGGTGGAG	720						
Db	661	CTGGAACATAGCGTCAAGGAGCGCGGGTCCCGCTGGCGCTGCCACGCCCGGGTGGAG	720						
Qy	721	GAGCGGGGGGAGTCCACGCGAAGTGTGCGGCGCGCGCTGTACCAGCTGCGCGCTGCCAC	780						
Db	721	GAGCGGGGGGAGTCCACGCGAAGTGTGCGGCGCGCGCTGTACCAGCTGCGCGCTGCCAC	780						
Qy	781	TGCCCTTGAGCCGAGCGGAGCGCGCTGGGAGGGGTCTGGGCCACCGCGGACGAG	840						
Db	781	TGCCCTTGAGCCGAGCGGAGCGCGCTGGGAGGGGTCTGGGCCACCGCGGACGAG	840						
Qy	841	CGGTGGACCGAGTGACCGTGGTTCCTGTGTGGTGTACCTGCCAGACCCCGGAAGAGC	900						
Db	841	CGGTGGACCGAGTGACCGTGGTTCCTGTGTGGTGTACCTGCCAGACCCCGGAAGAGC	900						
Qy	901	CACCTCTTTGGAGGGTGGCTCTCTGCGACGCGCCACTCCACCCATCGTGGGCGGCCA	960						
Db	901	CACCTCTTTGGAGGGTGGCTCTCTGCGACGCGCCACTCCACCCATCGTGGGCGGCCA	960						
Qy	961	GCACACGGGGCCCCCATCCACATCGCGGCCACACAGCTCCCTGGGACACGCTTCCTC	1020						
Db	961	GCACACGGGGCCCCCATCCACATCGCGGCCACACAGCTCCCTGGGACACGCTTCCTC	1020						

Db 2101 CCTGGACGATATCCACAGGCGCTGGGCGACCTTCGTGCTGCTGCGTGGGCGCCAGGACCC 2160
QY 2161 GCGCCCTGAGCTGTACTTTCTCAAGTGTGATGTGAGGGGCGGTGACGACACCATCCGCCA 2220
Db 2161 GCGCCCTGAGCTGTACTTTCTCAAGTGTGATGTGAGGGGCGGTGACGACACCATCCGCCA 2220
QY 2221 GGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG 2280
Db 2221 GGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG 2280
QY 2281 TCGGTATGCGGTGTGTCAGAGGCGCCCATGAGGCGGTGAGGCGGTTCAGAGCCCA 2340
Db 2281 TCGGTATGCGGTGTGTCAGAGGCGCCCATGAGGCGGTGAGGCGGTTCAGAGCCCA 2340
QY 2341 CGTCTCTACCTTGACAGACCTTCCAGCGGTATATCGGACGTGCTGCTGCTCATCTGCAGGA 2400
Db 2341 CGTCTCTACCTTGACAGACCTTCCAGCGGTATATCGGACGTGCTGCTGCTCATCTGCAGGA 2400
QY 2401 GACAGCGCGGTGAGGATGCGGTCTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG 2460
Db 2401 GACAGCGCGGTGAGGATGCGGTCTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG 2460
QY 2461 CAGTGGCTCTTTCAGCTCTTCTACGCTTCTATGTCGACGCTGCTGCTGCTGCTGCTGCTG 2520
Db 2461 CAGTGGCTCTTTCAGCTCTTCTACGCTTCTATGTCGACGCTGCTGCTGCTGCTGCTGCTG 2520
QY 2521 CAAGTCTCTACCTGACGAGGATGCGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2521 CAAGTCTCTACCTGACGAGGATGCGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
QY 2581 CAGCCTGTGCTACGCGCATGAGAGAACAGCTGTTGCGGGGATTCGCGGGGAGCGGCT 2640
Db 2581 CAGCCTGTGCTACGCGCATGAGAGAACAGCTGTTGCGGGGATTCGCGGGGAGCGGCT 2640
QY 2641 GCTCTGCTGTTGTTGGATGATTTCTGTTGCTGACACCTCACCTCACCCACGCGAAAC 2700
Db 2641 GCTCTGCTGTTGTTGGATGATTTCTGTTGCTGACACCTCACCTCACCCACGCGAAAC 2700
QY 2701 CTTCTCAGGACCTGCTGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Db 2701 CTTCTCAGGACCTGCTGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
QY 2761 GACAGTGTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
Db 2761 GACAGTGTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
QY 2821 GCGGCGCCAGCGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 2821 GCGGCGCCAGCGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
QY 2881 GCAGAGGACTACTCCAGTATGCGCGGACCTCCATCAGAGCCAGTCTCAGCTTCAACCG 2940
Db 2881 GCAGAGGACTACTCCAGTATGCGCGGACCTCCATCAGAGCCAGTCTCAGCTTCAACCG 2940
QY 2941 CGGCTTCAAGGCTGGAGGAAATCGCTGCGAACTCTTGGGCTTGGGCTGCTGCTGCTGCTGCTG 3000
Db 2941 CGGCTTCAAGGCTGGAGGAAATCGCTGCGAACTCTTGGGCTTGGGCTGCTGCTGCTGCTGCTG 3000
QY 3001 TCACAGCTGTTCTTCTGAGTTGAGGTGAACAGCTCCAGAGCGGTGCTGCTGCTGCTGCTGCTGCTG 3060
Db 3001 TCACAGCTGTTCTTCTGAGTTGAGGTGAACAGCTCCAGAGCGGTGCTGCTGCTGCTGCTGCTGCTG 3060
QY 3061 CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
Db 3061 CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
QY 3121 TCAGCAAGTTTGGAGAACCCACATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Db 3121 TCAGCAAGTTTGGAGAACCCACATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
QY 3181 CTGCTACTCTCTGAAGCAAGACGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240

Db 3181 CTGCTACTCTCTGAAGCCAGAACCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
QY 3241 CCGCCCTCTG 3300
Db 3241 CCGCCCTCTG 3300
QY 3301 GACTCGACACGCTGTACCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
Db 3301 GACTCGACACGCTGTACCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
QY 3361 GCTGAGTCTGGAAGTCTCCCGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
Db 3361 GCTGAGTCTGGAAGTCTCCCGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
QY 3421 ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480
QY 3481 GAGCAGACACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
Db 3481 GAGCAGACACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
QY 3541 CACACCCAGCGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
Db 3541 CACACCCAGCGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
QY 3601 CATGCTCGGCTGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
Db 3601 CATGCTCGGCTGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
QY 3661 GAGTGTCCAGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3720
Db 3661 GAGTGTCCAGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3720
QY 3721 GGGCCAGCTTTTCTCCTCACCAGGAGCGGCTTCCACTTCCACCATAGGAATAGTCCATCC 3780
Db 3721 GGGCCAGCTTTTCTCCTCACCAGGAGCGGCTTCCACTTCCACCATAGGAATAGTCCATCC 3780
QY 3781 CCAGATTCGCCATGTTTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
Db 3781 CCAGATTCGCCATGTTTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
QY 3841 AGGTGGAGACCTTGAGAGGACCTCTGGAGCTCTGGAAATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3900
Db 3841 AGGTGGAGACCTTGAGAGGACCTCTGGAGCTCTGGAAATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3900
QY 3901 CCCTGTACAGCGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
Db 3901 CCCTGTACAGCGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
QY 3961 GAGTGTGCTG 4015
Db 3961 GAGTGTGCTG 4015

RESULT 9

PCT-US99-06898-1
; Sequence 1, Application PC/TUS9906898
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: PCT/US99/06898
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618

EARLIER FILING DATE: 1997-10-01
EARLIER APPLICATION NUMBER: WO PCT/US/17885
EARLIER FILING DATE: 1997-10-01
EARLIER APPLICATION NUMBER: US 08/974,549
EARLIER FILING DATE: 1997-11-19
EARLIER APPLICATION NUMBER: US 08/974,584
EARLIER FILING DATE: 1997-11-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)...(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
PCT-US99-06898-1

Query Match 100.0%; Score 4015; DB 2; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTCGCTCTGCTGCGACGNGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 60
Db 1 GCAGCGCTCGCTCTGCTGCGACGNGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 60

QY 61 GCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 120
Db 61 GCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 120

QY 121 GCGCGTGGCCAGCTTGTGCGGGCCCTGGGGCCCAAGGGCTGGCGCTGGTCAGCGCG 180
Db 121 GCGCGTGGCCAGCTTGTGCGGGCCCTGGGGCCCAAGGGCTGGCGCTGGTCAGCGCG 180

QY 181 GGACCCGCGGGCTTTCGCGCGCTGTGTGCCAGTCCCTGGTGTGCTGCCCTGGACGC 240
Db 181 GGNCCGCGGGCTTTCGCGCGCTGTGTGCCAGTCCCTGGTGTGCTGCCCTGGACGC 240

QY 241 AGGCGCGCCCGCGCCCTCCCTTCGCGCCAGGTGTCTGCTGAAGAGGTGTGTGC 300
Db 241 AGGCGCGCCCGCGCCCTCCCTTCGCGCCAGGTGTCTGCTGAAGAGGTGTGTGC 300

QY 301 CCGAGTGTCTGAGAGCTGTGCGAGCGCGCGCGGAGAGAGCTGTGGCTTCGC 360
Db 301 CCGAGTGTCTGAGAGCTGTGCGAGCGCGCGCGGAGAGAGCTGTGGCTTCGC 360

QY 361 GTGTCTGGACGGGCGCGGGGCGCCCGCGAGGCTTTCACACAGAGCTGGCAGCTA 420
Db 361 GTGTCTGGACGGGCGCGGGGCGCCCGCGAGGCTTTCACACAGAGCTGGCAGCTA 420

QY 421 CTGTGCCAACACGGTGAACGACGCTGTGCGGGGAGCGGGGCTGTGCTGTGC 480
Db 421 CTGTGCCAACACGGTGAACGACGCTGTGCGGGGAGCGGGGCTGTGCTGTGC 480

QY 481 CCGCGTGGGCGACGCTGTGTGTACCTGTGGCAGCGTGGCGCTCTTTGTGTGT 540
Db 481 CCGCGTGGGCGACGCTGTGTGTACCTGTGGCAGCGTGGCGCTCTTTGTGTGT 540

QY 541 GGTCTCCAGCTGGCGCTACAGGTGTGCGGGCGCGCTGTACAGCTCGGCGCTGCCAC 600
Db 541 GGTCTCCAGCTGGCGCTACAGGTGTGCGGGCGCGCGCTGTACAGCTCGGCGCTGCCAC 600

QY 601 TCAGGCGCGCGCCCGCGCCACAGCTAGTGGACCCCGAAGCGCTGTGGATGCGAAGCG 660
Db 601 TCAGGCGCGCGCCCGCGCCACAGCTAGTGGACCCCGAAGCGCTGTGGATGCGAAGCG 660

QY 661 CTGGACCATAGCTCAGGAGCGCGGGTCCCTTGGCGCTGCCAGCGCGCGGTGCGAG 720
Db 661 CTGGACCATAGCTCAGGAGCGCGGGTCCCTTGGCGCTGCCAGCGCGCGGTGCGAG 720

QY 721 GAGGCGCGGGGAGTGTCCAGCGAAGTCTGCCGTTGCCAAGAGCGCTGCCGAGTGTGC 780
Db 721 GAGGCGCGGGGAGTGTCCAGCGAAGTCTGCCGTTGCCAAGAGCGCTGCCGAGTGTGC 780

Db 721 GAGGCGCGGGGAGTGTCCAGCGAAGTCTGCCGTTGCCAAGAGCGCCAGGGGTGGCG 780
QY 781 TGCCCTGAGCGGAGCGGACGCCCTTGGGAGGGGTCTGTGGCCCAACCCCGGCGAGAC 840
Db 781 TGCCCTGAGCGGAGCGGACGCCCTTGGGAGGGGTCTGTGGCCCAACCCCGGCGAGAC 840
QY 841 GCGTGGACGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 841 GCGTGGACGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 CACCTCTTTGGAGGGTGCCTCTCTGTGCACGCGCCACTCCACCCATCTCGTGGCGGCCA 960
Db 901 CACCTCTTTGGAGGGTGCCTCTCTGTGCACGCGCCACTCCACCCATCTCGTGGCGGCCA 960
QY 961 GCACACGCGGGCGCCCATCCACATCGCGGGCCACACAGTCCCTGTGGACACAGCTGTTC 1020
Db 961 GCACACGCGGGCGCCCATCCACATCGCGGGCCACACAGTCCCTGTGGACACAGCTGTTC 1020
QY 1021 CCGGCTGTACGCGGAGACCAAGCACTTCTCTACTCTCTAGGGGCAAGAGAGAGCTGG 1080
Db 1021 CCGGCTGTACGCGGAGACCAAGCACTTCTCTACTCTCTAGGGGCAAGAGAGAGCTGG 1080
QY 1081 GCGCTCTTCTCTACTCAGCTCTCTGAGGCGCCAGCTGACTTGGGCTCGGAGGCTCTGGA 1140
Db 1081 GCGCTCTTCTCTACTCAGCTCTCTGAGGCGCCAGCTGACTTGGGCTCGGAGGCTCTGGA 1140
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Db 1141 GACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGAGTTCGCCCGCTTCGCCCGCT 1200
QY 1201 GCGCCAGCGCTACTTGGCAATGCGGCCCTGTCTTCTGAGAGTCTTGGAGAGTCTGGA 1260
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QY 1261 GTGCCCTTACGGGGTCTCTCAAGACGACCTGCCGCTGCGAGCTGCGGTACCCCGAG 1320
Db 1261 GTGCCCTTACGGGGTCTCTCAAGACGACCTGCCGCTGCGAGCTGCGGTACCCCGAG 1320
QY 1321 AGCGGTGTCTGTGCCGGAGAACCCAGAGGCTCTGTGGCGGCGCCCGAGAGAGGA 1380
Db 1321 AGCGGTGTCTGTGCCGGAGAACCCAGAGGCTCTGTGGCGGCGCCCGAGAGAGGA 1380
QY 1381 CACAGACCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db 1381 CACAGACCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 CGGCTTGTGCGGGCGCTGCTGCGCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCGG 1500
Db 1441 CGGCTTGTGCGGGCGCTGCTGCGCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCGG 1500
QY 1501 CAACGAACGCGCTTCTCAGGAACACCAAGAGTTCATCTCCTCGGGAAGCATGCCAA 1560
Db 1501 CAACGAACGCGCTTCTCAGGAACACCAAGAGTTCATCTCCTCGGGAAGCATGCCAA 1560
QY 1561 GCTCTGCTGCGAGGAGTGAAGATGAGCGTGGGAGTGGGCTGCGCTGGCTGGCGAG 1620
Db 1561 GCTCTGCTGCGAGGAGTGAAGATGAGCGTGGGAGTGGGCTGCGCTGGCTGGCGAG 1620
QY 1621 GAGCCAGGGGTGGTGTGTTCCGCGCGCAGACACCGTCTGCTGAGGAGATCTTGGC 1680
Db 1621 GAGCCAGGGGTGGTGTGTTCCGCGCGCAGACACCGTCTGCTGAGGAGATCTTGGC 1680
QY 1681 CAAAGTCTGCACTGGCTGATGAGTGTACGCTCGAGCTGCTCAGGCTCTTTTCTTTT 1740
Db 1681 CAAAGTCTGCACTGGCTGATGAGTGTACGCTCGAGCTGCTCAGGCTCTTTTCTTTT 1740
QY 1741 TGTACGGAGACACCTTTCAAAGACAGGCTCTTTTCTTCTACCGAAGAGTCTCTGGAG 1800
Db 1741 TGTACGGAGACACCTTTCAAAGACAGGCTCTTTTCTTCTACCGAAGAGTCTCTGGAG 1800
QY 1801 CAAAGTGTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCCGAGTGT 1860
Db 1801 CAAAGTGTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCCGAGTGT 1860

Qy	1861	GGAAGCAGAGGT	CAGGCAGCATCGGAAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Dd	1861	GGAAGCAGAGGT	CAGGCAGCATCGGAAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Qy	1921	CTTCATCCCCAAGCCT	GACGGCTGCGGCCGATTGTGAACATGGAATGACTGCTGCTGGAGC	1980
Dd	1921	CTTCATCCCCAAGCCT	GACGGCTGCGGCCGATTGTGAACATGGAATGACTGCTGCTGGAGC	1980
Qy	1981	CAGAAGCTTCCG	CAGAGAAAAGGGCCGAGCGTCTCACTCGAGGGTGAAAGCACTGTT	2040
Dd	1981	CAGAACGTTCCG	CAGAGAAAAGGGCCGAGCGTCTCACTCGAGGGTGAAAGCACTGTT	2040
Qy	2041	CAGGGTCTCAACT	TACGAGGGGGCGGCCGCCCTCCTGGGGCCCTCTGTGCTGGG	2100
Dd	2041	CAGGGTCTCAACT	TACGAGGGGGCGGCCGCCCTCCTGGGGCCCTCTGTGCTGGG	2100
Qy	2101	CCTGGAGATATCAC	AGGGCCTGGGSCACTTCTGTCTCGTGTGGGGCCCGAGACC	2160
Dd	2101	CCTGGAGATATCAC	AGGGCCTGGGSCACTTCTGTCTCGTGTGGGGCCCGAGACC	2160
Qy	2161	GCGGCTGAGCTGT	TAAGGTGATGTGACGGGCGGTACGACACCACTCCGCCA	2220
Dd	2161	GCGGCTGAGCTGT	TAAGGTGATGTGACGGGCGGTACGACACCACTCCGCCA	2220
Qy	2221	GGACAGGCTCAG	GGAGGTCTATCGGCAGCATCATCAACCCCAGAACAGCTACTGCGTGG	2280
Dd	2221	GGACAGGCTCAG	GGAGGTCTATCGGCAGCATCATCAACCCCAGAACAGCTACTGCGTGG	2280
Qy	2281	TCGGTATGCGTGTCC	CAGAAAGCCGCCATGGCAGCTCCGCAAGGCCCTCAAGAGCCA	2340
Dd	2281	TCGGTATGCGTGTCC	CAGAAAGCCGCCATGGCAGCTCCGCAAGGCCCTCAAGAGCCA	2340
Qy	2341	CGTCTCTACCTT	CACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCAGGA	2400
Dd	2341	CGTCTCTACCTT	CACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCAGGA	2400
Qy	2401	GACCAAGCCGCT	GAGGATGCGTCTCATCGAGCAGAGCTCTCTCCTGAATGAGGCCAG	2460
Dd	2401	GACCAAGCCGCT	GAGGATGCGTCTCATCGAGCAGAGCTCTCTCCTGAATGAGGCCAG	2460
Qy	2461	CAGTGGCCTCTT	CGACGCTTCTTACGCTTTCATGTGCCACAGCGCCGTGCGCATCAGGGG	2520
Dd	2461	CAGTGGCCTCTT	CGACGCTTCTTACGCTTTCATGTGCCACAGCGCCGTGCGCATCAGGGG	2520
Qy	2521	CAAGTCTCTAGCT	TCAGTGCAGGGATCCCGCAGGGGTCCATCTCTPCCACGCTGCTCTG	2580
Dd	2521	CAAGTCTCTAGCT	TCAGTGCAGGGATCCCGCAGGGGTCCATCTCTPCCACGCTGCTCTG	2580
Qy	2581	CAGCCTCTGCT	TACGGGCACATGGAGAACAGCTGTTTTCGGGGATTCGGCGGACGGGCT	2640
Dd	2581	CAGCCTCTGCT	TACGGGCACATGGAGAACAGCTGTTTTCGGGGATTCGGCGGACGGGCT	2640
Qy	2641	GCTCCTCGGTTT	TGGTGATGATTTCTTGTGGTGACACCTCACCTCACCCACCGCAAAAC	2700
Dd	2641	GCTCCTCGGTTT	TGGTGATGATTTCTTGTGGTGACACCTCACCTCACCCACCGCAAAAC	2700
Qy	2701	CTTCCTCAGGAC	CCCTGTCGAGGTCTCCCTGAGTATGGTGGGTGAGTGAACCTGCGGAA	2760
Dd	2701	CTTCCTCAGGAC	CCCTGTCGAGGTCTCCCTGAGTATGGTGGGTGAGTGAACCTGCGGAA	2760
Qy	2761	GACAGTGGTGNA	CTTCCCTGTAGNAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Dd	2761	GACAGTGGTGNA	CTTCCCTGTAGNAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Qy	2821	GCCGGCCACG	CGCCTATTCGCCCTGGTGGGCCCTGCTGCTGATAACCGACCTTGAGGT	2880
Dd	2821	GCCGGCCACG	CGCCTATTCGCCCTGGTGGGCCCTGCTGCTGATAACCGACCTTGAGGT	2880
Qy	2881	GCAGAGCGACT	PACTCCAGCTATGCCCGAOCCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Dd	2881	GCAGAGCGACT	PACTCCAGCTATGCCCGAOCCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940

QY	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGCTCTTGGGCTCTTGGGCTGAAGTG	3000
DB	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGCTCTTGGGCTCTTGGGCTGAAGTG	3000
QY	3001	TCACAGCCTGTCTTCTGGATTGCAAGTGAAACAGCCTCCACAGCGTGTGCACCAACATCTA	3060
DB	3001	TCACAGCCTGTCTTCTGGATTGCAAGTGAAACAGCCTCCACAGCGTGTGCACCAACATCTA	3060
QY	3061	CAAGATCCTCCTGCTGCAGCGGTACAGTTTTCACGCAATGTGTGTCAGCTGCCATTTCA	3120
DB	3061	CAAGATCCTCCTGCTGCAGCGGTACAGTTTTCACGCAATGTGTGTCAGCTGCCATTTCA	3120
QY	3121	TCACGAAATTGGGAAGACCCACATTTTCTCGCGCTCATCTCTCACAGCGCTCCCT	3180
DB	3121	TCACGAAATTGGGAAGACCCACATTTTCTCGCGCTCATCTCTCACAGCGCTCCCT	3180
QY	3181	CTGCTACTCCATCCTGAAAGCCAAAGACGAGGATGTCGTGGGGCCCAAGGGCGCGC	3240
DB	3181	CTGCTACTCCATCCTGAAAGCCAAAGACGAGGATGTCGTGGGGCCCAAGGGCGCGC	3240
QY	3241	CGGGCCCTTGGCCCTCCAGGGCGGTGACGTGGCTGTGCACCAAGCATTTCTGTCAAGCT	3300
DB	3241	CGGGCCCTTGGCCCTCCAGGGCGGTGACGTGGCTGTGCACCAAGCATTTCTGTCAAGCT	3300
QY	3301	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGCTCACTCAGGACAGCCACAGCGCA	3360
DB	3301	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGCTCACTCAGGACAGCCACAGCGCA	3360
QY	3361	GCTGAGTGGAAAGTCCCGGGGACGACGTGACTGTGCCCTGGAGGCCGACCAACCCGCG	3420
DB	3361	GCTGAGTGGAAAGTCCCGGGGACGACGTGACTGTGCCCTGGAGGCCGACCAACCCGCG	3420
QY	3421	ACTGCCCTCAGACTTCAGAACCTTCCTGGACTGATGCCACCCGCCACACAGCCAGCGCA	3480
DB	3421	ACTGCCCTCAGACTTCAGAACCTTCCTGGACTGATGCCACCCGCCACACAGCCAGCGCA	3480
QY	3481	GAGCAGACACACAGACGCCCTGTACGCCGGGCTCTACGTCCACAGGAGGGGCGCGCC	3540
DB	3481	GAGCAGACACACAGACGCCCTGTACGCCGGGCTCTACGTCCACAGGAGGGGCGCGCC	3540
QY	3541	CACACCCAGGCCCGCCAGCGCTGGAGGCTTGAGGCCCTGAGTGAGTGTGGCCGAGGGCTG	3600
DB	3541	CACACCCAGGCCCGCCAGCGCTGGAGGCTTGAGGCCCTGAGTGAGTGTGGCCGAGGGCTG	3600
QY	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGGCT	3660
DB	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3661	GAGTGTCCAGACACTGTCCGCTTCTACATTCCCCACAGGCTGGGCTCGGGTCCACCCCA	3720
DB	3661	GAGTGTCCAGACACTGTCCGCTTCTACATTCCCCACAGGCTGGGCTCGGGTCCACCCCA	3720
QY	3721	GGGCCAGCTTTTCTCCACAGAGCCGGCTTCCACTCCCCACATAGGAATAGTTCATCC	3780
DB	3721	GGGCCAGCTTTTCTCCACAGAGCCGGCTTCCACTCCCCACATAGGAATAGTTCATCC	3780
QY	3781	CCAGATTGGCATTGTTCACCCCTCGCCCTGCCCTCTCTTTGCCCTTCCACCCCCACCATCC	3840
DB	3781	CCAGATTGGCATTGTTCACCCCTCGCCCTGCCCTCTCTTTGCCCTTCCACCCCCACCATCC	3840
QY	3841	AGGTGGAGACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGCACAAAGGTGTG	3900
DB	3841	AGGTGGAGACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGCACAAAGGTGTG	3900
QY	3901	CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTCTGGGTCAAAATGGGGG	3960
DB	3901	CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTCTGGGTCAAAATGGGGG	3960
QY	3961	GAGGTGCTGTGGGAGTAAAACTACATATATAGTATTTTTCAGTTTTTGAAGAAAA	4015
DB	3961	GAGGTGCTGTGGGAGTAAAACTACATATATAGTATTTTTCAGTTTTTGAAGAAAA	4015

Qy	1741	TGTCACGGAGACACAGT	TTCAAAGAACAAGGCTCT	TTTTTCTACCGAAGAGTGTCTGGAG	1800
Db	1741	TGTCACGGAGACACAGT	TTCAAAGAACAAGGCTCT	TTTTTCTACCGAAGAGTGTCTGGAG	1800
Qy	1801	CAAGTTTCAAGAAGCAT	TGGAAATCAGACAGCACT	TTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
Db	1801	CAAGTTTCAAGAAGCAT	TGGAAATCAGACAGCACT	TTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
Qy	1861	GGAAGCAGAGGT	CAGGACAGCATCGGGAAGCCAGGCGCGCCCT	GCTGACGTCCAGATCCG	1920
Db	1861	GGAAGCAGAGGT	CAGGACAGCATCGGGAAGCCAGGCGCGCCCT	GCTGACGTCCAGATCCG	1920
Qy	1921	CTTCATCCCAAGCCT	GACGGCTGCGGCCGATTTGTGAACATGACAT	TACGTCTGTGGGAGC	1980
Db	1921	CTTCATCCCAAGCCT	GACGGCTGCGGCCGATTTGTGAACATGACAT	TACGTCTGTGGGAGC	1980
Qy	1981	CAGAACGTTCCG	CAGAGAAAAGGGCCGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040	
Db	1981	CAGAACGTTCCG	CAGAGAAAAGGGCCGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040	
Qy	2041	CAGGGTCTCAACT	PACAGAGGGGGCGGCCCGCCCGGCTCCTGGGCGCTCTGTGCTGGG	2100	
Db	2041	CAGGGTCTCAACT	PACAGAGGGGGCGGCCCGCCCGGCTCCTGGGCGCTCTGTGCTGGG	2100	
Qy	2101	CCTGGACGATATCCAC	AGGCGCTTGGCGCACCTTCGTCTGCTGTCGTGGCGGCCCGAGACCC	2160	
Db	2101	CCTGGACGATATCCAC	AGGCGCTTGGCGCACCTTCGTCTGCTGTCGTGGCGGCCCGAGACCC	2160	
Qy	2161	CGCGCTTGAGCTGTAC	TTTGTCAAGGTGGATGTACGGGCGGTGTACGACACCATCCGCCA	2220	
Db	2161	CGCGCTTGAGCTGTAC	TTTGTCAAGGTGGATGTACGGGCGGTGTACGACACCATCCGCCA	2220	
Qy	2221	GGACAGGCTCACGGAGGT	TCATCGCCAGCATCATCAAAACCCAGAACAGTAC	TGCGTGGC	2280
Db	2221	GGACAGGCTCACGGAGGT	TCATCGCCAGCATCATCAAAACCCAGAACAGTAC	TGCGTGGC	2280
Qy	2281	TCGGTATGCCGTGGT	TCAGAAAGGCCGCCATAGGCGACGTCCGAAAGGCCCTTCAAGAGCCA	2340	
Db	2281	TCGGTATGCCGTGGT	TCAGAAAGGCCGCCATAGGCGACGTCCGAAAGGCCCTTCAAGAGCCA	2340	
Qy	2341	CGTCTCTACCTTGAC	ACACACTCCAGCCGTACATGCGACGTTCGTGGCTCACCTGCAGGA	2400	
Db	2341	CGTCTCTACCTTGAC	ACACACTCCAGCCGTACATGCGACGTTCGTGGCTCACCTGCAGGA	2400	
Qy	2401	GACCAGCCCGCTGAGG	GATCGCGTCTATCGACAGAGTCTCCTGATGAGGCCAG	2460	
Db	2401	GACCAGCCCGCTGAGG	GATCGCGTCTATCGACAGAGTCTCCTGATGAGGCCAG	2460	
Qy	2461	CAGTGGCTCTTCGAC	GTCTTCCTACGCTTCATGTCGCCACCGCGTGCATCAGGG	2520	
Db	2461	CAGTGGCTCTTCGAC	GTCTTCCTACGCTTCATGTCGCCACCGCGTGCATCAGGG	2520	
Qy	2521	CAAGTCTCTACGTCC	AGTCCAGGGGATCCCGCAGGGTCCCATCTCTCCACGCTGCTCTG	2580	
Db	2521	CAAGTCTCTACGTCC	AGTCCAGGGGATCCCGCAGGGTCCCATCTCTCCACGCTGCTCTG	2580	
Qy	2581	CAGCCTGTGTCACGG	CGACATGGAGAACAAAGCTGTTTTGCGGGGATTCGGCGGACGGGCT	2640	
Db	2581	CAGCCTGTGTCACGG	CGACATGGAGAACAAAGCTGTTTTGCGGGGATTCGGCGGACGGGCT	2640	
Qy	2641	GCTCCTCGT	TTGGTGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGGGAAAC	2700	
Db	2641	GCTCCTCGT	TTGGTGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGGGAAAC	2700	
Qy	2701	CTTCCTCAGGAC	CCCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAAC	2760	
Db	2701	CTTCCTCAGGAC	CCCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAAC	2760	
Qy	2761	GACAGTGGTGA	CTTCCTGTAGAGACGAGGCCCTGGGTGGCACGCTTTGTTTCAGAT	2820	
Db	2761	GACAGTGGTGA	CTTCCTGTAGAGACGAGGCCCTGGGTGGCACGCTTTGTTTCAGAT	2820	
Qy	2821	GCCGGCCACGGG	CCCTATTCCCTCGGTGGCGGCTGCTGCTGGATACCCGGACCTCGAGGT	2880	

[illegible]


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Db 3901 CCCTGTACACAGCGGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGG 3960
QY 3961 GAGGTGCTGTGGAGTAAATACTGAATATATAGAGTTTTTCAGTTTGAAGAAAA 4015
Db 3961 GAGGTGCTGTGGAGTAAATACTGAATATATAGAGTTTTTCAGTTTGAAGAAAA 4015

RESULT 11
PCT-US99-07160-1
; Sequence 1, Application PC/TUS9907160
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; APPLICANT: Geron Corporation
; APPLICANT: University Technology Corporation
; TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting
; FILE REFERENCE: 015389-003610PC
; CURRENT APPLICATION NUMBER: PCT/US99/07160
; EARLIER FILING DATE: 1999-03-31
; EARLIER FILING DATE: 1999-03-31
; EARLIER FILING DATE: 1996-10-01
; EARLIER APPLICATION NUMBER: US 08/724,643
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: US 08/844,419
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: US 08/846,017
; EARLIER FILING DATE: 1997-04-25
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,919
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-07160-1

Query Match 100.0%; Score 4015; DB 2; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGGTCTGCTGGCAGCTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCC 60
Db 1 GCAGCGCTGGTCTGCTGGCAGCTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCC 60

QY 61 GCAGCGCTGGTCTGCTGGCAGCTGGTCCCTGCTGGCAGCCACTACCGGAGTGCT 120
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Db 61 GCGCGTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCACCTACCGCGAGTGCT 120
QY 121 GCGGTGGCCACGTTTCGTGCGGCGCTGGGGCCCCAGGGCTGCGGCTGCTGACGCGG 180
Db 121 GCGGTGGCCACGTTTCGTGCGGCGCTGGGGCCCCAGGGCTGCGGCTGCTGACGCGG 180
QY 181 GGACCCGGCGGCTTTCCGGCGGCTGCTGGCCCAAGTCCCTGGTGGTGGCTGGCCAGCG 240
Db 181 GGACCCGGCGGCTTTCCGGCGGCTGCTGGCCCAAGTCCCTGGTGGTGGCTGGCCAGCG 240
QY 241 AGGGCGCCCGCCCGCCCGCCCTCCCTTCGCGCAGGTGCTGCTGCTCAAGGAGCTGTTGGC 300
Db 241 AGGGCGCCCGCCCGCCCGCCCTCCCTTCGCGCAGGTGCTGCTGCTCAAGGAGCTGTTGGC 300
QY 301 CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGGCGGAAAGAGTCTGCTGGCCTTCCGCTTCGC 360
Db 301 CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGGCGGAAAGAGTCTGCTGGCCTTCCGCTTCGC 360
QY 361 GCTGCTGGACGGGGCCCGGGGGCCCCCGCGAGGCTTTCACACAGAGCTGGCGAGCTA 420
Db 361 GCTGCTGGACGGGGCCCGGGGGCCCCCGCGAGGCTTTCACACAGAGCTGGCGAGCTA 420
QY 421 CTTGCCAACAACGCTGACGACGACTGCGGGGAGCGGGGCTGGGGCTGCTGCTGCG 480
Db 421 CTTGCCAACAACGCTGACGACGACTGCGGGGAGCGGGGCTGGGGCTGCTGCTGCG 480
QY 481 CCGGTGGGCGACGCTGCTGTTTACCTGTGTCAGCTGCGCGCTCTTTTGTGCTG 540
Db 481 CCGGTGGGCGACGCTGCTGTTTACCTGTGTCAGCTGCGCGCTCTTTTGTGCTG 540
QY 541 GGTCTCCAGCTGGCCCTACAGAGTGTGGGGGCGCGCTGTACCACTGGGCGCTGCCAC 600
Db 541 GGTCTCCAGCTGGCCCTACAGAGTGTGGGGGCGCGCTGTACCACTGGGCGCTGCCAC 600
QY 601 TCAGGCGCGGCCCCCGCCACACGCTAGTGGACCCGAAAGCGCTCTGGGATGCGAAGCGG 660
Db 601 TCAGGCGCGGCCCCCGCCACACGCTAGTGGACCCGAAAGCGCTCTGGGATGCGAAGCGG 660
QY 661 CTGGAACCATAGCGTCAGGAGGCGCGGGTCCCTTGGGCTGCCAGCCCGGGTGGCAG 720
Db 661 CTGGAACCATAGCGTCAGGAGGCGCGGGTCCCTTGGGCTGCCAGCCCGGGTGGCAG 720
QY 721 GAGGCGGGGGGAGTGCACAGCCGAAAGTGTGCGCTTGCCTAAGAGGCCAGGCGTGGCG 780
Db 721 GAGGCGGGGGGAGTGCACAGCCGAAAGTGTGCGCTTGCCTAAGAGGCCAGGCGTGGCG 780
QY 781 TGCCCTGTAGCCGAGCGGACGCGCTGTTGGGAGGGTCTGGGCGCCACCCGCGGAGGAC 840
Db 781 TGCCCTGTAGCCGAGCGGACGCGCTGTTGGGAGGGTCTGGGCGCCACCCGCGGAGGAC 840
QY 841 GCGTGACCGAGTGACCGTGGTTCCTGTGTGTGTACCTGCGCAGACCCCGCGAAGAGC 900
Db 841 GCGTGACCGAGTGACCGTGGTTCCTGTGTGTGTACCTGCGCAGACCCCGCGAAGAGC 900
QY 901 CACTCTTTGGAGGGTGGCTCTCTGCGACGCGCCACTCCACCCCATCCGTGGGCGGCCA 960
Db 901 CACTCTTTGGAGGGTGGCTCTCTGCGACGCGCCACTCCACCCCATCCGTGGGCGGCCA 960
QY 961 GCACACAGGGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTGCC 1020
Db 961 GCACACAGGGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTGCC 1020
QY 1021 CCGGTGTAGCGGAGACCAAGCACTTCCTTCTACTCCTCAGGCGACAAAGAGAGCTGCG 1080
Db 1021 CCGGTGTAGCGGAGACCAAGCACTTCCTTCTACTCCTCAGGCGACAAAGAGAGCTGCG 1080
QY 1081 GCCTCTTCTTCTACTAGCTCTCTGAGGCGCCAGCTGCTGCGGCTGCGAGGCTCGTGA 1140
Db 1081 GCCTCTTCTTCTACTAGCTCTCTGAGGCGCCAGCTGCTGCGGCTGCGAGGCTCGTGA 1140
QY 1141 GACCATCTTCTGGGTTCAGAGGCGCTGGATGCCAGGAGCTCCCGCGAGGTTGCCCGCCT 1200
Db 1141 GACCATCTTCTGGGTTCAGAGGCGCTGGATGCCAGGAGCTCCCGCGAGGTTGCCCGCCT 1200
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QY	1201	GC	CCCAAGCGCTACTGGCAAAATGCGGCCCTTGTTTCTGGAGACTGCTTGGGAACACACGGCA	1260
Db	1201	GC	CCCAAGCGCTACTGGCAAAATGCGGCCCTTGTTTCTGGAGACTGCTTGGGAACACACGGCA	1260
QY	1261	GT	CGCCCTACGGGTCGCTCTCAAGAGCACTGCCGCTCGAGCTCGCGTCAACCCAGC	1320
Db	1261	GT	CGCCCTACGGGTCGCTCTCAAGAGCACTGCCGCTCGAGCTCGCGTCAACCCAGC	1320
QY	1321	AG	CGGTGTCTGTGCCCGGAGAAGCCCAAGGCTCTGTGGCGCCCGCCAGAGAGGA	1380
Db	1321	AG	CGGTGTCTGTGCCCGGAGAAGCCCAAGGCTCTGTGGCGCCCGCCAGAGAGGA	1380
QY	1381	CAC	AGACCCCGCTGCTGTGACGTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGA	1440
Db	1381	CAC	AGACCCCGCTGCTGTGACGTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGA	1440
QY	1441	CG	CTTGTGCGGGCCTGCCTGCGCGCGGTGGTGGCCCCCAGGCGCTCTGGGGCTCCAGGA	1500
Db	1441	CG	CTTGTGCGGGCCTGCCTGCGCGCGGTGGTGGCCCCCAGGCGCTCTGGGGCTCCAGGA	1500
QY	1501	CAC	GAAGCGCGTTCCTCAGGACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA	1560
Db	1501	CAC	GAAGCGCGTTCCTCAGGACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1561	GC	TCTCGCTCAGGAGCTGACGTGGAAGATGAGCGTCGGGACTGGCGTTGGCTGGCGAG	1620
Db	1561	GC	TCTCGCTCAGGAGCTGACGTGGAAGATGAGCGTCGGGACTGGCGTTGGCTGGCGAG	1620
QY	1621	GAC	CCAGGGGTTGGCTGTGTTCCGGCCGACAGCACCGTCTCGGTGAGAGATCCTGGC	1680
Db	1621	GAC	CCAGGGGTTGGCTGTGTTCCGGCCGACAGCACCGTCTCGGTGAGAGATCCTGGC	1680
QY	1681	CA	AGTTCCTGCACCTGGCTGATGAGTGTACGTCTGTCGAGCTGCTCAGGTCCTTTCTTTA	1740
Db	1681	CA	AGTTCCTGCACCTGGCTGATGAGTGTACGTCTGTCGAGCTGCTCAGGTCCTTTCTTTA	1740
QY	1741	TG	TACGGAGACACCGTTTCAAAGAACACAGGCTCTTTTCTACCGGAAGAGTCTCGAG	1800
Db	1741	TG	TACGGAGACACCGTTTCAAAGAACACAGGCTCTTTTCTACCGGAAGAGTCTCGAG	1800
QY	1801	CA	AGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGTGCAGCTCGCGGAGCTGTC	1860
Db	1801	CA	AGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGTGCAGCTCGCGGAGCTGTC	1860
QY	1861	GGA	GCAGAGGTTCAGGCAGCATCGGGAAGCCAGGCGCGCCTCTGTCAGCTCCAGACTCCG	1920
Db	1861	GGA	GCAGAGGTTCAGGCAGCATCGGGAAGCCAGGCGCGCCTCTGTCAGCTCCAGACTCCG	1920
QY	1921	CT	TATCCCAACGCTCAGCGGCTGCGGCCGATGTGAACATGGACTACGTCGTGGGAGC	1980
Db	1921	CT	TATCCCAACGCTCAGCGGCTGCGGCCGATGTGAACATGGACTACGTCGTGGGAGC	1980
QY	1981	CAGA	ACCTTCGGCAGAAAAAGGGCCGAGCGTCTCACCTCGAGGTCGAAGGCACTGTT	2040
Db	1981	CAGA	ACCTTCGGCAGAAAAAGGGCCGAGCGTCTCACCTCGAGGTCGAAGGCACTGTT	2040
QY	2041	CAG	GTGCTCAACTACAGCGGGCGCGGCCCGCCGCTCCTGGCGCCTCTGTGCTGGG	2100
Db	2041	CAG	GTGCTCAACTACAGCGGGCGCGGCCCGCCGCTCCTGGCGCCTCTGTGCTGGG	2100
QY	2101	CT	TGGAGATCAACAGGCGCTGGCGACCTTCTGCTGCTGCGTGGCGCCAGGACCC	2160
Db	2101	CT	TGGAGATCAACAGGCGCTGGCGACCTTCTGCTGCTGCGTGGCGCCAGGACCC	2160
QY	2161	GCG	CCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCATCCGCCA	2220
Db	2161	GCG	CCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCATCCGCCA	2220
QY	2221	GG	ACGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2280
Db	2221	GG	ACGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2280

QY	2281	TCGGTATGCGGTGGTCCAGAAAGCCGCCCATGGGACAGCTCCGCAAGAGCCCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCGGTGGTCCAGAAAGCCGCCCATGGGACAGCTCCGCAAGAGCCCTTCAAGAGCCA	2340
QY	2341	CGTCTACCTTTGACAGACCTCCAGCCGTACATGCGACAGTTTCGTGGCTCACCTCGAGGA	2400
Db	2341	CGTCTACCTTTGACAGACCTCCAGCCGTACATGCGACAGTTTCGTGGCTCACCTCGAGGA	2400
QY	2401	GACACGCCGCTGAGGGATGCCCTGCTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG	2460
Db	2401	GACACGCCGCTGAGGGATGCCCTGCTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG	2460
QY	2461	CAGTGGCTCTTCGACGCTCTTCCTACGCTTCATGTGCCACACCGCTGGCATCAGGG	2520
Db	2461	CAGTGGCTCTTCGACGCTCTTCCTACGCTTCATGTGCCACACCGCTGGCATCAGGG	2520
QY	2521	CAAGTCTACGTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTACGTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
QY	2581	CAGCCTGTCTACGGCAGATGAGAACACAGCTGTTTGGGGATTCGGCGGACACGGCT	2640
Db	2581	CAGCCTGTCTACGGCAGATGAGAACACAGCTGTTTGGGGATTCGGCGGACACGGCT	2640
QY	2641	GCTCCTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGCGAAAC	2700
Db	2641	GCTCCTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGCGAAAC	2700
QY	2701	CTTCTCAGACACCTGGTCCGAGGTGTCCTGTAGTATGGCTGGTGGTGAACCTTGGGAA	2760
Db	2701	CTTCTCAGACACCTGGTCCGAGGTGTCCTGTAGTATGGCTGGTGGTGAACCTTGGGAA	2760
QY	2761	GACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCAGACGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCAGACGGCTTTTGTTCAGAT	2820
QY	2821	GCGGGCCACCGGCTATPTCCCTTGGTGCGCCTGTCTGTGGATCCCGGACCCCTGGAGGT	2880
Db	2821	GCGGGCCACCGGCTATPTCCCTTGGTGCGCCTGTCTGTGGATCCCGGACCCCTGGAGGT	2880
QY	2881	GCAGAGGACTACTCCAGCTATGCCGGACCTCCATCAGAGCAGCTCTACCTTCAACCG	2940
Db	2881	GCAGAGGACTACTCCAGCTATGCCGGACCTCCATCAGAGCAGCTCTACCTTCAACCG	2940
QY	2941	CGGTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGTCTTCGGGTGAAGTG	3000
Db	2941	CGGTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGTCTTCGGGTGAAGTG	3000
QY	3001	TCACAGCCTCTTCTGGATTTGAGGTGAACAGCCTCCACAGCTGTCACCAACATCTA	3060
Db	3001	TCACAGCCTCTTCTGGATTTGAGGTGAACAGCCTCCACAGCTGTCACCAACATCTA	3060
QY	3061	CAAGATCCTCTGTGTCAGGCGTACAGGTTTTCAGCATGTGTGTCAGCTCCCATTTCA	3120
Db	3061	CAAGATCCTCTGTGTCAGGCGTACAGGTTTTCAGCATGTGTGTCAGCTCCCATTTCA	3120
QY	3121	TCAGCAGTTTGGAAACCCACATTTTCTCTGGGGTCTATCTCTGACAGGGCTCCCT	3180
Db	3121	TCAGCAGTTTGGAAACCCACATTTTCTCTGGGGTCTATCTCTGACAGGGCTCCCT	3180
QY	3181	CTGCTACTCCTCTGAAAGCCAAAGACGAGGGATGTCTGCTGGGGCCAAAGGCGCGC	3240
Db	3181	CTGCTACTCCTCTGAAAGCCAAAGACGAGGGATGTCTGCTGGGGCCAAAGGCGCGC	3240
QY	3241	CGGCCCCCTGCCCTCCAGGCGGTGACAGTGTGTGCCACCAAGCATTCCTGTCTCAAGCT	3300
Db	3241	CGGCCCCCTGCCCTCCAGGCGGTGACAGTGTGTGCCACCAAGCATTCCTGTCTCAAGCT	3300
QY	3301	GACTCGACACGGTGTACCTACGTGCGACCTCTGGGGTCACTCAGGACGCCAGAGCA	3360
Db	3301	GACTCGACACGGTGTACCTACGTGCGACCTCTGGGGTCACTCAGGACGCCAGAGCA	3360
QY	3361	GCTGAGTCTGGAAGCTCCCGGGAGCAGCGCTGACTGCCCTGGAGCCGCGCAACCCGCG	3420

Qy	241	ACGGCCGCCGCCGCCGCCGCCCTTCCTTCGCCCAGGTGTCTTGCTGAAGAGCTGTGGC	300
Db	241	ACGGCCGCCGCCGCCGCCGCCCTTCCTTCGCCCAGGTGTCTTGCTGAAGAGCTGTGGC	300
Qy	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCGC	360
Db	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCGC	360
Qy	361	GCTGCTGGACGGGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	420
Db	361	GCTGCTGGACGGGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	420
Qy	421	CCTGCCCAACACAGGTGACACGACACTGCGGGGGAGCGGGGGCTGSGGGCTGCTGCTGG	480
Db	421	CCTGCCCAACACAGGTGACACGACACTGCGGGGGAGCGGGGGCTGSGGGCTGCTGCTGG	480
Qy	481	CCGCGTGGGGACGACGTGCTGTGCTTACCTGCTGGCAGCGTGCGCCTCTTTGTGTGT	540
Db	481	CCGCGTGGGGACGACGTGCTGTGCTTACCTGCTGGCAGCGTGCGCCTCTTTGTGTGT	540
Qy	541	GGCTCCAGCTGGCGCTTACCAGTGTGCGGGCGCGCGCTGTACACGCTCGGCCCTGCCAC	600
Db	541	GGCTCCAGCTGGCGCTTACCAGTGTGCGGGCGCGCGCTGTACACGCTCGGCCCTGCCAC	600
Qy	601	TCAGGCCCGGCCGCCACACGCTAGTGTGACCCCGAAGCGTCTGGAGTCGCAACGGGC	660
Db	601	TCAGGCCCGGCCGCCACACGCTAGTGTGACCCCGAAGCGTCTGGAGTCGCAACGGGC	660
Qy	661	CTGGAACCATAGGCTCAGGAGGCGGGGTCCCTCTGGGGCTGCACGCCGGGTGCGAG	720
Db	661	CTGGAACCATAGGCTCAGGAGGCGGGGTCCCTCTGGGGCTGCACGCCGGGTGCGAG	720
Qy	721	GAGCGCGGGGAGTGCACAGCGAAGTCTGCGTTGCCCAAGAGGCCACAGGCGTGGCGC	780
Db	721	GAGCGCGGGGAGTGCACAGCGAAGTCTGCGTTGCCCAAGAGGCCACAGGCGTGGCGC	780
Qy	781	TGCCCTTGAGCGGAGCGGACGCCCTGTGGGCAAGGGTCTTGCGGCCACCCGGGCAAGGAC	840
Db	781	TGCCCTTGAGCGGAGCGGACGCCCTGTGGGCAAGGGTCTTGCGGCCACCCGGGCAAGGAC	840
Qy	841	CGGTGACCGAGTGACCGTGGTTCTGTGTGTGTGTACCTGCCAGACCCGCCCAAGAACG	900
Db	841	CGGTGACCGAGTGACCGTGGTTCTGTGTGTGTGTACCTGCCAGACCCGCCCAAGAACG	900
Qy	901	CACCTCTTTGGAGGGTGGCTCTCTGCGACGCGGCCACTCCACCCATPCCTGTGGGCGGCCA	960
Db	901	CACCTCTTTGGAGGGTGGCTCTCTGCGACGCGGCCACTCCACCCATPCCTGTGGGCGGCCA	960
Qy	961	GCACGCGGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACACGCTGTGTC	1020
Db	961	GCACGCGGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACACGCTGTGTC	1020
Qy	1021	CCCGGTGTACCCGAGACCAAGCACTTCCTCTACTCTCAGGGGACAAAGGAGCAGTGTGG	1080
Db	1021	CCCGGTGTACCCGAGACCAAGCACTTCCTCTACTCTCAGGGGACAAAGGAGCAGTGTGG	1080
Qy	1081	GCCCTCTCTTCTACTCAGTCTCTGAGGCGCCAGCCTGACTGTGGGCTCGGAGGCTGTGGA	1140
Db	1081	GCCCTCTCTTCTACTCAGTCTCTGAGGCGCCAGCCTGACTGTGGGCTCGGAGGCTGTGGA	1140
Qy	1141	GACCATCTTTCTGGTTTCCAGGCCCTTGATGCCAGGGACTCCCGCAGGTTGCCCGCCT	1200
Db	1141	GACCATCTTTCTGGTTTCCAGGCCCTTGATGCCAGGGACTCCCGCAGGTTGCCCGCCT	1200
Qy	1201	GCCCCAGCGCTACTGCGAAATGCGGGCCCCCTGTTCCTGAGGTGCTGTGGGAACACCGCCA	1260
Db	1201	GCCCCAGCGCTACTGCGAAATGCGGGCCCCCTGTTCCTGAGGTGCTGTGGGAACACCGCCA	1260
Qy	1261	GTGCCCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGGAGCTCGGCTCACCCACG	1320
Db	1261	GTGCCCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGGAGCTCGGCTCACCCACG	1320
Qy	1321	AGCCGGTGTCTGTGCCCCGGGAGAACCCCAAGGCTCTGTGGCGGCCCCCGAGGAGGAGA	1380

Db	1321	AGCCGCTGCTGTGCCGCGAGAAAGCCCAAGGCGCTCTGTGGCGGCCCCCGAGGAGGGA	1380
QY	1381	CACAGACCCCGCTCGCCTGTGTGACGTGTCTCCGCCACAGACAGACGCCCCCTGGCAGGTGA	1440
Db	1381	CACAGACCCCGCTCGCCTGTGTGACGTGTCTCCGCCACAGACAGACGCCCCCTGGCAGGTGA	1440
QY	1441	CGGCTTCGTGCGGGGCTGCCTGCGCGCGCTGTGGTGGTGGCCCCAGGCGCTCTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCGTGCGGGGCTGCCTGCGCGCGCTGTGGTGGTGGCCCCAGGCGCTCTGGGGCTCCAGGCA	1500
QY	1501	CAACGAACCGCGTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGGAAGCATGCCAA	1560
Db	1501	CAACGAACCGCGTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGGAAGCATGCCAA	1560
QY	1561	GCTCTCGTCGACGAGCTGACGTGGAAGATGACGCTGCGGAGCTGCCTTTGGCTGCGCAG	1620
Db	1561	GCTCTCGTCGACGAGCTGACGTGGAAGATGACGCTGCGGAGCTGCCTTTGGCTGCGCAG	1620
QY	1621	GAGCCACAGGGTTGGCTGTCTCCGCGCCGACAGACACCGCTGCTGTCGAGAGATCCTGGC	1680
Db	1621	GAGCCACAGGGTTGGCTGTCTCCGCGCCGACAGACACCGCTGCTGTCGAGAGATCCTGGC	1680
QY	1681	CAAGTTCTCTGCACCTGCGTATGATGTGTACGTCTGTCGAGCTGCTCAGGCTCTTCTTTA	1740
Db	1681	CAAGTTCTCTGCACCTGCGTATGATGTGTACGTCTGTCGAGCTGCTCAGGCTCTTCTTTA	1740
QY	1741	TGTCACGGAGACACGTTTCAAAGAACACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
Db	1741	TGTCACGGAGACACGTTTCAAAGAACACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGCAGCTGCGGAGCTGTC	1860
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGCAGCTGCGGAGCTGTC	1860
QY	1861	GGAACAGAGGTCAGGCAGCATCGGGAAGCAGGCGCCGCTGCTGTCAGCTCCAGACTCGG	1920
Db	1861	GGAACAGAGGTCAGGCAGCATCGGGAAGCAGGCGCCGCTGCTGTCAGCTCCAGACTCGG	1920
QY	1921	CTTCATCCCCAAGCCTCAGCGGCTGCGCGCGATTTGAAATGAGACTACGCTGTGGGAGC	1980
Db	1921	CTTCATCCCCAAGCCTCAGCGGCTGCGCGCGATTTGAAATGAGACTACGCTGTGGGAGC	1980
QY	1981	CAGAACGTTCCGACAGAAAAAGGGGCGGAGCGTCTCACCCTCAGAGGCTGAAGGCACGTGT	2040
Db	1981	CAGAACGTTCCGACAGAAAAAGGGGCGGAGCGTCTCACCCTCAGAGGCTGAAGGCACGTGT	2040
QY	2041	CAGCGTCTCAACTACGAGCGGGCGCGCGCCGCTCCTGGCGCGCTCTGTGCTGGG	2100
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QY	2101	CCTGGACGATATCCACAGGCGCTGGCGCACTTCGTCGTGGTGTGGGGGCCACAGGACCC	2160
Db	2101	CCTGGACGATATCCACAGGCGCTGGCGCACTTCGTCGTGGTGTGGGGGCCACAGGACCC	2160
QY	2161	GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTACGCGGCGCTACGACACCATCCCCA	2220
Db	2161	GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTACGCGGCGCTACGACACCATCCCCA	2220
QY	2221	GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGCTACCTCGTGGC	2280
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QY	2281	TCGGTATGCGGTGTCAGAAAGCGCCCATGGCAGCTGCGGAAGGCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCGGTGTCAGAAAGCGCCCATGGCAGCTGCGGAAGGCTTCAAGAGCCA	2340
QY	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTACCTGCAGGA	2400
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTACCTGCAGGA	2400
QY	2401	GACCACCGCGTGAGGAGTCCGTGTCATCGAGCAGAGCTCTCCTGCTGAATGAGGCCAG	2460
Db	2401	GACCACCGCGTGAGGAGTCCGTGTCATCGAGCAGAGCTCTCCTGCTGAATGAGGCCAG	2460

Db 2401 GACCAGCCGCTGAGGATGCGTCTCATCGAGCAGAGCTCTCCCTGAATGAGCCAG 2460
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Db 2461 CAGTGGCCCTTCGACGCTTCCTAGGCTTCATGTGCCACACAGCGCGTGGCAGCATCAGGGG 2520
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Db 2521 CAAGTCTACGTCCAGTGCACGGGATCCGAGGGCTCCATCCCTCCACGCTGCTCTG 2580
QY 2581 CAGCCTGTCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCT 2640
Db 2581 CAGCCTGTCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCT 2640
QY 2641 GCTCTGCGCTTGGTGGATGATTTCTGTGTGACACCTCAGCTCACCACCGCGAAAC 2700
Db 2641 GCTCTGCGCTTGGTGGATGATTTCTGTGTGACACCTCAGCTCACCACCGCGAAAC 2700
QY 2701 CTTCTTCAGGACCCCTGGTCCGAGGTGCTCCTGAGTATGCTGCGTGGTGAACCTTGGGAA 2760
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QY 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACAGCGCCCTCCCT 3180
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QY 3181 CTGCTACTCATCTGAAAGCCAGAACGACGAGGATGCTGGGGCCCAAGGGCCGCG 3240
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QY 3301 GACTGCACACCGTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
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QY 3421 ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3481 GAGCAGACACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3481 GAGCAGACACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540

QY 3541 CACACCCAGCCCGCAGCCGCTGGAGTCTGAGGCCCTGAGTGAAGTGTGGCCGAGGCGCTG 3600
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QY 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
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QY 3661 GAGTGTCCAGCACACCTGCGCTTTCACCTTCCACAGGCTGCGGCTGCGGCTCACCACCA 3720
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RESULT 13

US-09-052-864-1
; Sequence 1, Application US/09052864
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; TITLE OF INVENTION: Variants
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,864
; FILING DATE: 31-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0033000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION:
OTHER INFORMATION: transcriptase (tHTR)*
US-09-052-864-1

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Query Match	100.0%;	Score	4015;	DB	15;	Length	4015;
Best Local Similarity	100.0%;	Pred.	No.	0;			
Matches	4015;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	GCAGCGTGGTCTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCGCCACCCCGCGATGCC	60				
Db	1	GCAGCGTGGTCTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCGCCACCCCGCGATGCC	60				
Qy	61	CGCGCTCCCGCTGCGAGCCGTGCTCCCTGCTGGCAGCCACTACCGCGAGGTGCT	120				
Db	61	CGCGCTCCCGCTGCGAGCCGTGCTCCCTGCTGGCAGCCACTACCGCGAGGTGCT	120				
Qy	121	CGCGCTGGCCACGTTCTGCGCGCCCTGGGCCCCCAGGGCTGGCGGCTGGCGACGCGGG	180				
Db	121	CGCGCTGGCCACGTTCTGCGCGCCCTGGGCCCCCAGGGCTGGCGGCTGGCGACGCGGG	180				
Qy	181	GGACCCGGCGCTTTCCGGCGCGTGGTGCCCACTGCTGTGCGTGCCCTGGGACGC	240				
Db	181	GGACCCGGCGCTTTCCGGCGCGTGGTGCCCACTGCTGTGCGTGCCCTGGGACGC	240				
Qy	241	ACGGCCGCCCGCCCGCCCTCTCTCCGCCAGGTGTCCTGCTGAAGAGCTTGGTGGC	300				
Db	241	ACGGCCGCCCGCCCGCCCTCTCTCCGCCAGGTGTCCTGCTGAAGAGCTTGGTGGC	300				
Qy	301	CCGAGTGTGTGACAGGCTGTGCGAGCGCGCGAAGAACGTGTGGCTTCGCGCTTCGC	360				
Db	301	CCGAGTGTGTGACAGGCTGTGCGAGCGCGCGAAGAACGTGTGGCTTCGCGCTTCGC	360				
Qy	361	GCTGCTGGACGGGGCCCGGGGGCCCCCGAGGCCCTTACCAACACGCGTGGCAGCTA	420				
Db	361	GCTGCTGGACGGGGCCCGGGGGCCCCCGAGGCCCTTACCAACACGCGTGGCAGCTA	420				
Qy	421	CCTGCCCAACAGGTGACCGACGCACTCGGGGGAGCGGGGCGTGGGGGCTGCTCTGCG	480				
Db	421	CCTGCCCAACAGGTGACCGACGCACTCGGGGGAGCGGGGCGTGGGGGCTGCTCTGCG	480				
Qy	481	CCGCTGGGCGACGACGTCGTGGTGTACCTGCTGGCAGCTGCGCGCTTTTGTGCTGGT	540				
Db	481	CCGCTGGGCGACGACGTCGTGGTGTACCTGCTGGCAGCTGCGCGCTTTTGTGCTGGT	540				

QY	541	GGCTCCACGCTGGCCCTACCAAGGTGTGGGGCCGCGCTGTACCAAGCTCGGGCGTGCAC	600
DB	541	GGCTCCACGCTGGCCCTACCAAGGTGTGGGGCCGCGCTGTACCAAGCTCGGGCGTGCAC	600
QY	601	TCAGGCGCGCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAAAGGCG	660
DB	601	TCAGGCGCGCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAAAGGCG	660
QY	661	CTGGAACCATAGGCTCAGGGAGGCGGGGTCCCTCTGGGCTTCAGACCCCGGGTGCAG	720
DB	661	CTGGAACCATAGGCTCAGGGAGGCGGGGTCCCTCTGGGCTTCAGACCCCGGGTGCAG	720
QY	721	GAGGCGGGGCGAGTGCAGCGGAAGTCTGCGTTGCCAAGAGGCCCAGGCGTGGCG	780
DB	721	GAGGCGGGGCGAGTGCAGCGGAAGTCTGCGTTGCCAAGAGGCCCAGGCGTGGCG	780
QY	781	TGCCCCGTAGCGGAGCGAGCGCCGTTGGGAGGGTCTCTGGGCCACCCGGGAGGAC	840
DB	781	TGCCCCGTAGCGGAGCGAGCGCCGTTGGGAGGGTCTCTGGGCCACCCGGGAGGAC	840
QY	841	CGCTGACCGAGTGACCGTGGTTCTGTGTGTTCACCTGCCAGCCCGCGAAGAGC	900
DB	841	CGCTGACCGAGTGACCGTGGTTCTGTGTGTTCACCTGCCAGCCCGCGAAGAGC	900
QY	901	CACCTCTTTGGAGGGTGGCTCTCTGGCACGGGCCACTCCCACCCTCCGTGGGCGCA	960
DB	901	CACCTCTTTGGAGGGTGGCTCTCTGGCACGGGCCACTCCCACCCTCCGTGGGCGCA	960
QY	961	GCACGCGGGGCCCCCATCCACATCGGGGCCACCACTGCTGGGACAGCCCTGTCC	1020
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DB	1021	CCGGGTGTAGCGGAGCAAGCACTTCTCTACTCTCAGGCGCAAGGAGCAGTGG	1080
QY	1081	GGCTCTCTTCTACTAGCTCTCTGAGGCCAGCCCTGACTGGGCTCGSAGGCTGTGGA	1140
DB	1081	GGCTCTCTTCTACTAGCTCTCTGAGGCCAGCCCTGACTGGGCTCGSAGGCTGTGGA	1140
QY	1141	GACCATCTTCTGGTGTCCAGGCGCTTGATGCCAGGAGACTTCCCGCAGGTTGCCCGCT	1200
DB	1141	GACCATCTTCTGGTGTCCAGGCGCTTGATGCCAGGAGACTTCCCGCAGGTTGCCCGCT	1200
QY	1201	GGCCCCAGGCTACTGGCAATAGCGGCCCTGTGTGGAGCTGCTTGGGAACACACGCA	1260
DB	1201	GGCCCCAGGCTACTGGCAATAGCGGCCCTGTGTGGAGCTGCTTGGGAACACACGCA	1260
QY	1261	GTGCCCCCTAGGGGTGCTCTCAAGAGCACTGCCGCTCGAGCTCGGCTCACCCAGC	1320
DB	1261	GTGCCCCCTAGGGGTGCTCTCAAGAGCACTGCCGCTCGAGCTCGGCTCACCCAGC	1320
QY	1321	AGCCGGTGTCTGTGCCCGGAGAGCCCAAGGCTCTGTGGCGCCGCCAGGAGGA	1380
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QY	1381	CACAGACCCCGTCCCTGTGTGAGTGTCTCGGCACACAGAGTTCATCTCCCTGGGGAAGCATGCCAA	1440
DB	1381	CACAGACCCCGTCCCTGTGTGAGTGTCTCGGCACACAGAGTTCATCTCCCTGGGGAAGCATGCCAA	1440
QY	1441	CGGCTCTGTGGGGCTGCTCTGCGCGGCTGGTGCCCGCAGGCTCTGGGGCTCCAGGCA	1500
DB	1441	CGGCTCTGTGGGGCTGCTCTGCGCGGCTGGTGCCCGCAGGCTCTGGGGCTCCAGGCA	1500
QY	1501	CAACGAACCGCGTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1560
DB	1501	CAACGAACCGCGTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1561	GCTCTCGCTCAGGAGCTGAGCTGGAAGATGAGCTGCGGAGCTTGGCTTGGCTGGCAG	1620
DB	1561	GCTCTCGCTCAGGAGCTGAGCTGGAAGATGAGCTGCGGAGCTTGGCTTGGCTGGCAG	1620
QY	1621	GAGCCCCAGGGTGTGGCTGTGTTCGGGCCGAGACAGCCGCTCGCTGAGGAGATCTCGC	1680

Db	1621	GAGCCGAGGGTGGCTGTTCGCGCCGAGAGCACCGTCTCGGTGAGGAGATCTGGC	1680
QY	1681	CRAAGTTCTGCACTGGCTGATGAGTGTACGTCGTCGAGCTCTCAGAGTCTTTCTTTTA	1740
Db	1681	CRAAGTTCTGCACTGGCTGATGAGTGTACGTCGTCGAGCTCTCAGAGTCTTTCTTTTA	1740
QY	1741	TGTCAGGAGAGACCAGCTTTCAAGAACAAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
Db	1741	TGTCAGGAGAGACCAGCTTTCAAGAACAAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1801	CRAAGTTGCAAGCATTTGGAATCAGACAGACATTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
Db	1801	CRAAGTTGCAAGCATTTGGAATCAGACAGACATTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCGG	1920
Db	1861	GGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCGG	1920
QY	1921	CTTATCCCAAGCCTGACGGCTGGCGCGATTTGAACATGGAGTACGTCGTGGGAGC	1980
Db	1921	CTTATCCCAAGCCTGACGGCTGGCGCGATTTGAACATGGAGTACGTCGTGGGAGC	1980
QY	1981	CAGAACGTTCCGAGAGAAAGAGGGCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTCCGAGAGAAAGAGGGCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTGTCAACTACGAGCGGGCGCGCCCGCCCTCTGGGCGCTCTGTGTGGG	2100
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QY	2101	CTTGGACGATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGCTGCTGCTGCTGCTG	2160
Db	2101	CTTGGACGATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGCTGCTGCTGCTGCTG	2160
QY	2161	GCCGCTGAGCTGTACTTTGTCGAAGTGGATGTGACGGCGCGTACGACACCATCCCCCA	2220
Db	2161	GCCGCTGAGCTGTACTTTGTCGAAGTGGATGTGACGGCGCGTACGACACCATCCCCCA	2220
QY	2221	GGACAGGCTCAGGAGGTGATGCCAGCATCATCAAAACCCAGAACACAGTACTGCTGGG	2280
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QY	2341	CGTCTCTACTTGCACAGACTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
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QY	2401	GACCAGCCGCTGAGGGATGCCGTCTCATCGAGCAGAGTCTCCCTGAATGAGGCCAG	2460
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QY	2461	CAGTGGCTCTTCGAGCTTCTCAGCTTCATGTCGCACACGCGCTGCGCATCAGGG	2520
Db	2461	CAGTGGCTCTTCGAGCTTCTCAGCTTCATGTCGCACACGCGCTGCGCATCAGGG	2520
QY	2521	CAAGTCTACGTCCAGTGCAGGGATCCGCGAGGCTCCATCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTACGTCCAGTGCAGGGATCCGCGAGGCTCCATCTCTCCACGCTGCTCTG	2580
QY	2581	CAGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
Db	2581	CAGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
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Db	2641	GCTCTGCGTGTGGTGGATGATTTCTTGTGTTGAGACCTTCACCTCACCCACGCGAAAC	2700
QY	2701	CTTCTCAGAGCCCTGCGAGGTGTCCTTCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2760
Db	2701	CTTCTCAGAGCCCTGCGAGGTGTCCTTCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2760
Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAGACAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAGACAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
QY	2821	GCCGGCCACAGGCTTATTCCTTGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
Db	2821	GCCGGCCACAGGCTTATTCCTTGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
QY	2881	GCAGAGGACTACTCCAGCTTATCCCGGACCTCCATCAGAGCCAGTCTCACCCTTCAACCG	2940
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Db	2941	CGCTTCAAGGCTGGAGGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3000
QY	3001	TCACAGGCTGTTTCTGGATTTGAGGTGAACAGCCCTCCAGACGGTGTGCACCAACATCTA	3060
Db	3001	TCACAGGCTGTTTCTGGATTTGAGGTGAACAGCCCTCCAGACGGTGTGCACCAACATCTA	3060
QY	3061	CAAGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3120
Db	3061	CAAGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3120
QY	3121	TCAGCAAGTTTGAAGAACCACATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3180
Db	3121	TCAGCAAGTTTGAAGAACCACATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3180
QY	3181	CTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3240
Db	3181	CTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3240
QY	3241	CGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3300
Db	3241	CGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3300
QY	3301	GACTGACACCGTGTCACTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3360
Db	3301	GACTGACACCGTGTCACTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3360
QY	3361	GCTGAGTCCGGAAGCTCCCGGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3420
Db	3361	GCTGAGTCCGGAAGCTCCCGGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3420
QY	3421	ACTGCTCTCAGACTTCAAGACCATCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3480
Db	3421	ACTGCTCTCAGACTTCAAGACCATCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3480
QY	3481	GAGCAGACACAGCAGCCTTGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3540
Db	3481	GAGCAGACACAGCAGCCTTGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3540
QY	3541	CAGACCCAGGCTCCGACCGCTGGAGTGTGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTG	3600
Db	3541	CAGACCCAGGCTCCGACCGCTGGAGTGTGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTG	3600
QY	3601	CATGTCCGGCTGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3660
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3660
QY	3661	GAGTGTCCAGCAGCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3720
Db	3661	GAGTGTCCAGCAGCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3720
QY	3721	GGGCCAGCTTTTCTCACCAGGAGCCGGCTTCCACTCCCAATAGGAAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCTCACCAGGAGCCGGCTTCCACTCCCAATAGGAAATAGTCCATCC	3780
QY	3781	CCAGATTCGCCATTTGTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3840
Db	3781	CCAGATTCGCCATTTGTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3840

QY 3841 AGGTGGAGACCTGAGAGGACCTGGGAGCTGGGAATTTGGAGTGACCAAAAGGTGTG 3900
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RESULT 14
US-09-402-181A-1
; Sequence 1, Application US/09402181A
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US/09/402,181A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Aussenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-0026200S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hprt"
; /note= "human telomerase reverse
; transcriptase (hprt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-402-181A-1
Query Match 100.0%; Score 4015; DB 21; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCGCTCGCTCCTGCTGCGCAGCTGGGAAGCCCTGCCCGCCGCCACCCCGCGATGCC 60
Db 1 GCAGCGCTCGCTCCTGCTGCGCAGCTGGGAAGCCCTGCCCGCCGCCACCCCGCGATGCC 60
QY 61 GCGCGCTCCCGCTGCCGAGCCGCTCCCTGCTGCGCAGCCACTACCCGAGAGTGT 120
Db 61 GCGCGCTCCCGCTGCCGAGCCGCTCCCTGCTGCGCAGCCACTACCCGAGAGTGT 120
QY 121 GCCGCTGCGCACAGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTGACAGCGG 180
Db 121 GCCGCTGCGCACAGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTGACAGCGG 180
QY 181 GGACCCGCGCGCTTTCGCGCGCTGGTGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 GGACCCGCGCGCTTTCGCGCGCTGGTGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 ACGCCCGCCCCCGCCCGCCCTCTTCCGCCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 ACGCCCGCCCCCGCCCGCCCTCTTCCGCCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 CCGAGTGTGCGAGAGGCTGTCGAGCGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 CCGAGTGTGCGAGAGGCTGTCGAGCGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 361 GCTGCTGGACGGGGCGCGGGGGCGCCCGCCCGAGCGCTTACACACAGCGTGGCGGCGGCGG 420
Db 361 GCTGCTGGACGGGGCGCGGGGGCGCCCGCCCGAGCGCTTACACACAGCGTGGCGGCGGCGG 420
QY 421 CCTGCCCAACACAGGTGACCGACGACGCTGCGGGGGAGCGGGGGCGTGGGGGCTGTGCTGCG 480
Db 421 CCTGCCCAACACAGGTGACCGACGACGCTGCGGGGGAGCGGGGGCGTGGGGGCTGTGCTGCG 480
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QY 601 TCAGGCGCGGGCGG 660
Db 601 TCAGGCGCGGGCGG 660
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QY 721 GAGCGCGGGGGCAGTGCCAGCCGAAAGTCTCCGCTTGCCCAAGAGGCGCCAGGCGTGGCGG 780
Db 721 GAGCGCGGGGGCAGTGCCAGCCGAAAGTCTCCGCTTGCCCAAGAGGCGCCAGGCGTGGCGG 780
QY 781 TGCCCCCTGAGCGGAGCGGCGCGCGTGGCGAGGGTCTCTGGCGCCACCCCGCGGCGAGAC 840
Db 781 TGCCCCCTGAGCGGAGCGGCGCGCGTGGCGAGGGTCTCTGGCGCCACCCCGCGGCGAGAC 840

QY	841	CGCTGGACCGAGTCACCGTGGTTCTCTGTGTGGTGTCACTGTGCCAGACCCCGCCGAAGAAGC	900	Db	1921																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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D	b		3001	TCACAGCCTGTTTCTCGATTTGCAGGTGAACAGCCTCCAGCAGGGTGTCACCACAATCTA	3060
Q	y		3061	CAAGATCCTCCTGCTGCAGCGTACAGGTTTTCACGATGTGTGCTGCAGCTCCCATTTCA	3120
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Q	y		3181	CTGCTACTCCTACTCTAAAGCCAAAGAACGACGAGGATGTCTGCTGGGGCCCAAGGCCGCC	3240
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Q	y		3241	CGGCCCTCTGCCCTCCGAGCGCTGTCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
D	b		3241	CGGCCCTCTGCCCTCCGAGCGCTGTCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
Q	y		3301	GACTCGACACCGTGTACCTTACCTGCCACTCTTGGGTCACTCAGACAGCCCGACAGCA	3360
D	b		3301	GACTCGACACCGTGTACCTTACCTGCCACTCTTGGGTCACTCAGACAGCCCGACAGCA	3360
Q	y		3361	GCTGAGTFCGAAGCTCCCGGGGACGACGCTGTACTGCTGAGGCGCGCACCAACCCGCC	3420
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D	b		3421	ACTGCCCTCAGACTTCAAGACCACTCTGGACTGATGCCACCCGCCACAGCCAGCCGA	3480
Q	y		3481	GACGACACACGACGCGCTGCACCGGGCTCTACGTCCCAGGAGGAGGGGGCGGC	3540
D	b		3481	GACGACACACGACGCGCTGCACCGGGCTCTACGTCCCAGGAGGAGGGGGCGGC	3540
Q	y		3541	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCGCTG	3600
D	b		3541	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCGCTG	3600
Q	y		3601	CATGTCGGGTGAAGGCTGAGTGTCCGGCTGAGGCGTGAAGGCTGAGGATGTCCAGCCAAAGGCT	3660
D	b		3601	CATGTCGGGTGAAGGCTGAGTGTCCGGCTGAGGCGTGAAGGCTGAGGATGTCCAGCCAAAGGCT	3660
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Q	y		3721	GGGCCAGCTTTCCTCACCAGGACCCGGCTTCCACTCCCCACATAGGAATAAGTCCATCC	3780
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Q	y		3781	CCAGATTCCGCAATTGTTACCCCTCGCCCTGCGCTCCTTTGCGTTCACCCCGACATCC	3840
D	b		3781	CCAGATTCCGCAATTGTTACCCCTCGCCCTGCGCTCCTTTGCGTTCACCCCGACATCC	3840
Q	y		3841	AGGTGGAGACCTTGACGAAGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG	3900
D	b		3841	AGGTGGAGACCTTGACGAAGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG	3900
Q	y		3901	COCTGTACAGCGCAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAATTTGGGG	3960
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RESULT 15
US-09-402-181B-1
; Sequence 1, Application US/09402181B
; ; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
;

2

Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, William B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181B
 FILING DATE: 29-Sep-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
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 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-00262005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
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 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454
 OTHER INFORMATION: /product= "hTERT"
 /note= "human telomerase reverse
 transcriptase (hTERT) catalytic protein
 component"
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 TS-09-402-181B-1

	Query Match	100.0%	Score 4015;	DB 21;	Length 4015;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 4015;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GCACGCTGGCTCTGCTGGCGACGTGGGAAGCCTGGCCCGCGCCACCCCGGATGCC	60		
Db	1	GCACGCTGGCTCTGCTGGCGACGTGGGAAGCCTGGCCCGCGCCACCCCGGATGCC	60		

QY 61 GCGCGTCCCGTCCGAGCGTGGCTCCCTGCTGCGAGGCCACTACCGGAGGTGCT 120
DB 61 GCGCGTCCCGTCCGAGCGTGGCTCCCTGCTGCGAGGCCACTACCGGAGGTGCT 120
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DB 121 GCGCTGGCCACGTTGCTGGCGCGCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGG 180
QY 181 GGACCGGGGGTTCCTGGCGCGCTGGTGGCCAGTGCCTGGTGGTGGCTGGGACGC 240
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DB 361 GCTGTGGAGCGGGGGCCCCCGAGGCTTACACACAGAGCTGCGCAGCTA 420
QY 421 CTTGCCACACAGGTACGACGCTGCGGGGGAGCGGGGGCTGCTGCTGGC 480
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VERSION 1
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
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Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing By: Washington University
Genome Sequencing Center
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AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished

COMMENT Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr

Plate: 99 row: E column: 07

High quality sequence stop: 492.

Location/Qualifiers

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ACCESSION BG917907.1 GI:14298383

VERSION EST.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 851)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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Library constructed by Life Technologies Investigator

providing samples: Jeffrey Green, M.D., NIH

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Db 278 TACTCAGGTATGCCCGACGCTCAATTAAGACGAGCTTCACCTTCCAGAGGTGTTTCAAA 337

QY 2951 GCTGGGAGAACATGCGTGCAGAACTCTTTGGGGTCTTTGGGGTGAAGTGTGCAGAGCGTG 3010

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Db      338 GCTGGGAGACCAATCGGACACAGCTCCCTGTCGGTCTTCGGGTGAAGTGTACGGTCTCA 397
QY      3011 TTCTCGATTTCCAGGTGACACGCTCCAGAGCGTGTGCACCAACATCTACAGATCCCTC 3070
Db      398 TTCTAGACTTGCAGTGAACAGCTCCAGACAGCTGTCATCAATATATACAGATCTTC 457
QY      3071 CTGCTCCAGCGGTACAGGTTTCCAGCATGTGTGCTCAGTCCAGTCCCATTTTCATCAGCAAGTT 3130
Db      458 CTGCTTCAGGCTTACAGGTTCCATGATGTGTGATTCAGCTTCCCTTTGACCAAGCGTGT 517
QY      3131 TGAAGAACCCACATTTTCTGCGCTCATCTCTGACAGCGCTCCCTCTGCTACTCTC 3190
Db      518 AGAAGAACTCACAATCTTCTGGGCATCACTCCAGCAAGCATCTCTGCTGCTATGCT 577
QY      3191 ATCTGAAAGCCAGCAAGGATGTCTGCTGGGGGCCAAAGCGCCGCCGCCCTCTG 3250
Db      578 ATCTGAAGTCAAGAATCAGGAATGACACTAAAGGCTCTGGCTC-----CIT 627
QY      3251 CCTCCAGGCGGTGAGTGGCTGTGCCACCAAGCAATTCCT-GCTCAAGCTGACTCGACA 3309
Db      628 TCTCTGAAGCGGACATTTGGCTCTGTACAGGCTTCTGCTCAAGCTGGCTGCTCA 687
QY      3310 CGGTGTCACCTAGTCCACTCTCTGGGTCTCACTCAGCAGAGCCAGCAGCTGAGTCG 3369
Db      688 TTCTGTCTACAAATGTCTCTGGGACCTCTGAGAGCAGCCCAAAACCGTGTGCCG 747
QY      3370 GAAGTCCCGGGGACGCTGACTGCCCTGGAGCGCAGCCAAACCGCACTGCCCTC 3429
Db      748 GAAGTCCGAGAGCGACAATGACCATGCTTACAGCTGCAGCTGACCCAGCCAGCAAGGAC 807
QY      3430 AGACTTCAAGACCATCTCTGGACTGA 3454
Db      808 AGACTTTCAGGACCAATTGGGACTAA 832

RESULT 6
AW276315/c
LOCUS   AW276315
DEFINITION   xr10b12.x1 NCI_CGAP_Lu28 416 bp mRNA linear EST 03-JAN-2000
           mRNA sequence.
ACCESSION   AW276315
VERSION     AW276315.1 GI:6663345
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 416)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgaps-r@mail.nih.gov
           Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
           Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
           Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
           I.M.A.G.E. Consortium DNA Sequencing by: Washington University
           Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           www-bio.llnl.gov/obpr/image/image.html
           Seq primer: -40UP from Gibco
           High quality sequence stop: 413.
FEATURES    Location/Qualifiers
             1..416
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2759711"
             /tissue_type="two pooled squamous cell carcinomas"
             /lab_host="DH10B"

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/clone_lib="NCI_CGAP_Lu28"
/Note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies."
BASE COUNT 90 a 118 c 130 g 78 t
ORIGIN

Query Match 10.4%; Score 416; DB 9; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-72;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3594 AGSCCTGCATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCC 3653
Db      416 AGSCCTGCATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCC 357
QY      3654 AAGGGCTGAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGAGCTGCGCTCGGCTC 3713
Db      356 AAGGGCTGAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGAGCTGCGCTCGGCTC 297
QY      3714 CACCCAGGGCCAGCTTTTCTCACCAGAGAGCCGGCTTCCATCTCCCCACATAGGAATAG 3773
Db      296 CACCCAGGGCCAGCTTTTCTCACCAGAGAGCCGGCTTCCATCTCCCCACATAGGAATAG 237
QY      3774 TCCATCCCGAGATTCGCCATTTGTCACCCCTGCGCTCGGCTTCCATCTCCCCACATAGGAATAG 3833
Db      236 TCCATCCCGAGATTCGCCATTTGTCACCCCTGCGCTCGGCTTCCATCTCCCCACATAGGAATAG 177
QY      3834 ACCATCCAGTGTGAGAGACCTTGAGAGAGACCTTGGAGAGCTGCGGAATTTTGGAGTGACCAA 3893
Db      176 ACCATCCAGTGTGAGAGACCTTGAGAGAGACCTTGGAGAGCTGCGGAATTTTGGAGTGACCAA 117
QY      3894 AGGTGTGCCCTGTACACAGCGAGAGACCTTGACACCTGGAGTGGGGTCCCTGTGGGTCAA 3953
Db      116 AGGTGTGCCCTGTACACAGCGAGAGACCTTGACACCTGGAGTGGGGTCCCTGTGGGTCAA 57
QY      3954 TTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATAGTATATAGTATTTTTCAGTTTGA 4009
Db      56 TTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATAGTATATAGTATTTTTCAGTTTGA 1

RESULT 7
AW281296
LOCUS   AW281296
DEFINITION   zt08g02.r1 NCI_CGAP_GCB1 389 bp mRNA linear EST 14-AUG-1997
           mRNA sequence.
ACCESSION   AW281296
VERSION     AW281296.1 GI:1924194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 389)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgaps-r@mail.nih.gov
           This clone is available royalty-free through LNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Insert Length: 2187 Std Error: 0.00
           Seq primer: -28ml3 rev2 ET from Amersham
           High quality sequence stop: 385.
FEATURES    Location/Qualifiers
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             /organism="Homo sapiens"
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             /db_xref="taxon:9606"
             /clone="IMAGE:712562"
             /tissue_type="germinal center B cell"
             /lab_host="DH10B"
             /clone_lib="NCI_CGAP_GCB1"

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Db 121 CGCGCTCCTCGTTGCCCGCGGTGGCTCTCTCTGCTGGCAGCGATACCGGGAGGTGTGG 180
 Qy 122 CCCTGTCACAGTTCGTGGCGCCCTGGGGCCCGAGGCTGGCGGTGGTGCACGCGGG 181
 Db 181 CCCTGTCACAGTTCGTGGCGCCCTGGGGCCCGAGGCTGGCGGTGGTGCACGCGGG 240
 Qy 182 GACCGCGCGCTTTCGCGCGCTGGTGGCCAGTGCCTGCTGGCTGGCGCTGGGACGA 241
 Db 241 GACCGCGCGCTTTCGCGCGCTGGTGGCCAGTGCCTGCTGGCTGGCGCTGGGACGA 300
 Qy 242 CGCGCGCGCCCGCGCGCCCTCTCTCCGCGAGGTGCTGCTGGAAGAGCTGGTGGCC 301
 Db 301 CAGCTCCACCTCGCGACCTTCTCTCCACAGGTGTCATCCCTGAAGAGCTGGTGGCC 360
 Qy 302 CGAGTGTGTCAGAGGTGTCGAGCGCGCGCGGAGAACGTGTGGCTTCGCTTCGCG 361
 Db 361 AGGTTGTGTCAGAGTCTCGAGCGCGCACGAGAGAACGTGTGGCTTCGCTTCGCG 420
 Qy 362 CTGCTGGAGCG 421
 Db 421 CTGCTTAACAGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 Qy 422 CTGCGCAACAGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
 Db 481 TTGCGCAACAGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 Qy 482 CGCGTGGCGCGAGCGTGTGTTACCTGCTGCGACGCTGCGCGCTTCTTGTGCTGG 539
 Db 541 CGAGTGGCGCGAGCGTGTGTTACCTGCTGCGACGCTGCTCTTATCTCTGCG 598

RESULT 9

BQ258274

LOCUS

DEFINITION NISC_kp11g04.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
 IMAGE:5409222, mRNA sequence.

ACCESSION

BQ258274

VERSION

BQ258274.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 664)

NCI-CCGAP

http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cyapbs-remail.nih.gov

CDNA Library Preparation: J. Baker (Stanford University)

DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium/LLNL

Sequencing Center (NISC)

Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov

MGI:1845958

Plate: LLAM12043

Seq primer: Sp6 primer.

Location/Qualifiers

1..664

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CD-1"

/db_xref="taxon:10090"

/clone="IMAGE:5409222"

/tissue_type="embryo, late gastrula"

/dev_stage="embryo, 7.5 dpc"

/lab_host="XLI-Blue"

/clone_lib="Baker mouse embryo e7.5"

/note="Vector: pCS105; Site:1: NotI; Site:2: SalI; cDNA

made by oligo-dr priming. Directionally cloned into

FEATURES

source

RESULT 10

AA811084/c

LOCUS

DEFINITION

oa85c05.s1 NCI_CGAP_GCB1

Homo sapiens

cDNA clone

IMAGE:1319048 3',

mRNA sequence.

AA811084

VERSION

AA811084.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 340)

Query Match 7.9%; Score 317.8; DB 13; Length 664;
 Best Local Similarity 68.3%; Pred. No. 5.2e-53;
 Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;
 BASE COUNT 155 a 177 c 183 g 149 t
 ORIGIN

Qy 1108 GCCCAGCTCAGCTGGCCCTCGGAGGCTCGTGGAGACCATCTTCTGCGGTTCAGGCCCTG 1167
 Db 9 GCCTTAACCTGACTGGGCGCAGGAGACTGGTGGAGATCATCTTCTTGGGCTCAAGGCCCTAG 68
 Qy 1168 GATGCCAGGACTCCCGCAGGTTGCCCGCTGCCCGCAGCGCTACTGGCAATGCGGCC 1227
 Db 69 GACATCAGGACCACCTCGCAGGACACACCGCTCTATCCGTCGATACGTGCGAGATGCCGCC 128
 Qy 1228 CTTGTTTCTGGAGTGTCTGGGAACACGCGCAGTGCCTTACGGGTGCTCTCAAGAC 1287
 Db 129 CTTGTTTCAACAGCTGCTGGTGAACCATGCGAGAGTGCCAATATGTCAAGACTCCTTCAGGTC 188
 Qy 1288 GCACCTGCGCTGGGAGCTGGGTGTCACCCAGCAGCGGTGTCGTGTCGCCGGGAGAGCC 1347
 Db 189 ACATTGCAAGTTTCGAACACGCAAAACACAGGTGACAGATGCCCT----- 232
 Qy 1348 CCAGGGCTCTGTGCGCGCCCGCGAGGAGGAGGACACAGCCCGCTGCGCTGGTGCAGCT 1407
 Db 233 -----TGAACCCAGCCACCGCACCTCATGTGATTT 263
 Qy 1408 GCTCCCGCAGCACAGCAGCCCTGGCAGGTGTACGGCTTGTGCGGGCCTGCTGCGCGC 1467
 Db 264 GCTCCCGCTGCACAGCAGTCCCTGGCAGGTATATGTTTCTTCCGGGCTGTCTCTGAA 323
 Qy 1468 GCTGCTCCCGCAGGCTCTGGGGCTCAGGACCAACAGAGCCGCTTCTTCAGGACAC 1527
 Db 324 GGTGGTGTCTGTAGTCTCTGGGGTACCGGCAACATGAGCGCGCTTCTTAAAGAACTT 383
 Qy 1528 CAAGAAGTTCATCTCCCTGGGAGAGCATGCCAAGCTCTGCTGCGAGGAGCTGAGCTGAA 1587
 Db 384 AAAGAAGTTCATCTCTGTTGGGAATATCGGCAAGCTATCACTGCGAGAACTGATGTGAA 443
 Qy 1588 GATGAGCGTGGGAGCTGCGCTGGGTGCGCAGAGCCCGAGGGGTGGCTGTGTCGCGC 1647
 Db 444 GATGAAGTAGAGGATTGCCACTGGCTCCGCGCAGCAGGAGGAGGAGGAGGAGGAGG 503
 Qy 1648 CGCAGACACCGTCTGCTGAGGAGATCCTTGGCCAAAGTCTTGCACCTGGCTGATGAGTGT 1707
 Db 504 TGCAGAGCACCGTCTGAGGAGAGGATCCTTGGCTACGTTCTGTTCTGGTGTGAGACAC 563
 Qy 1708 GTACGTGCTGAGCTGCTCAGGTCTTCTTTTATGTACGAGGAGACACAGTTTCAAAAGAA 1767
 Db 564 ATACGTGGTACAGCTGCTTAGGTCTTTTATCATCAGAGAGACACATTCACAGAGAA 623
 Qy 1768 CAGGCTCTTTTCTTACCGAAGAGTGTCTGAGCAAGTTTC 1808
 Db 624 CAGGCTCTTCTTACCGTAAGAGTGTGTGGAGCAAGCTGC 664

AA811084 340 bp mRNA linear EST 19-FEB-1998
 oa85c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319048 3',
 mRNA sequence.
 AA811084
 AA811084.1 GI:2880695
 EST.
 HOMO SAPIENS
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 340)

AUTHORS TITLE JOURNAL COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 2249 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 331.

FEATURES source

1..340
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1319048"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_GCB1"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-).
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTGAAGTGGGCGCGCTCCATTTTTTTTTTTT-3'
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT ORIGIN

Query Match 7.6%; Score 305.4; DB 9; Length 340;
Best Local Similarity 99.1%; Pred. No. 1.3e-50;
Matches 328; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
3685 TCACCTCCCCACAGGCTGGCGCTCGGCTCCACCCCGAGGCGCCAGCTTTCTCCACAGGAG 3744
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340 TCACCTCCCCACAGG-TGGCGCTCGGCTCCACCCCGAGGCGCCAGCTTTCTCCACAGGAG 282
3745 CCGGGTTCACCTCCACATAGGAATAGTCCATCCCGAGATCCGCATGTTCACCCCT 3804
|||||
281 CCGCGCTTCACCTCCCGACATAGGAATAGTCCATCCCGAGATTCGCCATGTTCACCCCT 222
|||||
3805 CGCCCTGCCCTCCTTGGCTCCACCCCGACCATCCAGTGGAGACCCCTGAGAGGACCC 3864
|||||
221 CGCCCTGCCCTCCTTGGCTCCACCCCGACCATCCAGTGGAGACCCCTGAGAGGACCC 162
3865 TGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTGTACAGCGGAGGACCCCTG 3924
|||||
161 TGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTGTACAGCGGAGGACCCCTG 102
3925 CACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGGAGGTGCTGTGGAGTAAATACT 3984
|||||
101 CACCTGGATGGGGGT-CCTGTGGGTCAAAATTTGGGGGAGGTGCTGTGGAGTAAATACT 43
3985 GAATATATAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGT 4015
|||||
42 GAATATATAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGT 12

RESULT 11

BB651920
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BB651920 614 bp mRNA linear EST 26-OCT-2001
BB651920 RIKEN full-length enriched, ES cells Mus musculus cDNA
clone C33020G14 5', mRNA sequence.
BB651920
BB651920.1 GI:16486058
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 614)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okada
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
, D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
, Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
, K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES source

1..614
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C33020G14"
/cell_type="ES cells"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, ES cells"
/note="Site.1: XhoI; Site.2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTTTTT 3'], cDNA was

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGACAGAGATTCGCGATTAATTAATATCCGCCGCCGCC 3']".

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BASE COUNT      93 a 191 c 188 g 142 t
ORIGIN

Query Match      7.2%; Score 290.8; DB 10; Length 614;
Best Local Similarity 74.7%; Pred. No. 1.2e-47;
Matches 378; Conservative 0; Mismatches 127; Indels 1; Gaps 1;

QY 2 CAGCGCTGGTCTGCTGGCAGCTGGGAGACCTTGGCCCGCCGACACCCCGCGATGCCG 61
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Db 61 CACCCTTGCACTTGGTTCCCGCACGTGGGAGGCCCATCCCGGCTTGAGCAATGACC 120
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QY 62 CCGCTGCCCGCTGGCGAGCGCTGGCTCCCTGCTGCGCAGCACCTACCGCGAGGTGCTG 121
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Db 121 CCGCTGCTGCTGGCCCGGCTGGCTCTGCTGCGCAGCGCATACCGGAGGTGCTG 180
   || || || || || || || || || || || || || || || || || || || || ||
QY 122 CCGCTGGCCACGTTGCTGGCGGCGCTGGGGCCCCAGGGCTGCGGCTGGTGCAGCGCGG 181
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Db 181 CCGCTGGCAACCTTTGTGGCGGCGCTGGGGCCCCGAGGCGAGCGGCTTGCAACCCGG 240
   || || || || || || || || || || || || || || || || || || || || ||
QY 182 GACCCGGGCGCTTCCGCGCGCTGGTGGCCGAGTGGCTGGTGGTGGTGGTGGTGG 241
   || || || || || || || || || || || || || || || || || || || || ||
Db 241 GACCCGAAGATCATCCGCACTTGGTTGGTGGCCCAATGCTAGTGTGATGCACTGGG 300
   || || || || || || || || || || || || || || || || || || || || ||
QY 242 CGCGCGCCCGCCCGCGCCCGCTTCCGCGCAGGTGCTGCTGAAGAGAGTGGTGGCC 301
   || || || || || || || || || || || || || || || || || || || || ||
Db 301 CAGCCTCCACCTGCGGACCTTTCCTTCCACAGAGTGTATCCCTGNAAGAGTGGTGG 360
   || || || || || || || || || || || || || || || || || || || || ||
QY 302 CGAGTGTCTCAGAGGTGTGCGAGCGCGCGCGAAGACGTGCTGCGCTTCGCTTCGCG 361
   || || || || || || || || || || || || || || || || || || || || ||
Db 361 AGGGTGTGCGAGAGCTCTCGAGCGCAACGAGAGAACGTGCTGCTTTGGCTTTGAG 420
   || || || || || || || || || || || || || || || || || || || || ||
QY 362 CTGCTGGAGGGGCGCGCGGCGCGCGCGCGAGGCTTCAACACAGCGCTGCGCTAC 421
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Db 421 CTGCTTAACGAGGCGAGGCGGCGCTCCCTCCTGCTGCTGCTGCTGCTGCTGCTG 480
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QY 422 CTGCGCCAAACAGGTGACCCAGCACCTGCGGGGGGAGCGGCGCTGCGGCTGCTGCTG 481
   || || || || || || || || || || || || || || || || || || || || ||
Db 481 TTGCCCAACACATGTTATGAGACCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
   || || || || || || || || || || || || || || || || || || || || ||
QY 482 CCGGT-GGCGGACGAGTCTGCTGCTC 506
   || || || || || || || || || || || || || || || || || || || || ||
Db 541 CGAGTGGGCGGACGACCTGCTGGGTC 566
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```

```

RESULT 12
AA748707/c 315 bp mRNA linear EST 18-FEB-1998
LOCUS ny02e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270592 3',
DEFINITION mRNA sequence.
ACCESSION AA748707
VERSION AA748707.1 GI:2788665
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapps-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

```

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html
 Insert length: 1226 Std Error: 0.00
 Seq primer: -40ml3 fwd. Et from Amersham
 High quality sequence stop: 281.

FEATURES

source

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1..315
Location/Qualifiers
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/clone_lib="NCI_CGAP_GCB1"

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/note="Vector: pT7n3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTGGAGCGCGCCCTCATTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

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BASE COUNT      68 a 95 c 87 g 65 t
ORIGIN

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Query Match      7.1%; Score 284.4; DB 9; Length 315;
Best Local Similarity 96.2%; Pred. No. 1.9e-46;
Matches 302; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 3703 GCGCTCGGCTCACCCAGGCGCAGCTTTCTCACCAGAGCGCGCTTCACATCCCA 3762
   || || || || || || || || || || || || || || || || || || || || ||
Db 314 GCGCTCGGCTCACCCAGGCGCAGCTTTCTCACCAGAGCGCGCTTCACATCCCA 255
   || || || || || || || || || || || || || || || || || || || || ||
QY 3763 CATAGAAATAGTCCATCCCATCCAGATTCGATTTTCCACCCCTGCGCTCCCTTCG 3822
   || || || || || || || || || || || || || || || || || || || || ||
Db 254 CATAGAAATAGTCCATCCCATCCAGATTCGATTTTCCACCCCTGCGCTCCCTTCG 195
   || || || || || || || || || || || || || || || || || || || || ||
QY 3823 CTTC-ACCCCAACCATCCAGTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAAT 3881
   || || || || || || || || || || || || || || || || || || || || ||
Db 194 GGCGCGGCGCCACCATCCAGTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAAT 135
   || || || || || || || || || || || || || || || || || || || || ||
QY 3882 TGGAGTGACCAAGGTGTCCTGTACACAGGGGAGGACCTTGACCTGGATGGGGGTCC 3941
   || || || || || || || || || || || || || || || || || || || || ||
Db 134 TGGAGTGACCAAGGTGTCCTGTACACAGGGGAGGACCTTGACCTGGATGGGGGTCC 75
   || || || || || || || || || || || || || || || || || || || || ||
QY 3942 CTGTGGTCAAAATTTGGGGGAGGTGCTGTGGAGTAAATACATGAATATATAGTTTTC 4001
   || || || || || || || || || || || || || || || || || || || || ||
Db 74 CTGTGGTCAAAATTTGGGGGAGGTGCTGTGGAGTAAATACATGAATATATAGTTTTC 15
   || || || || || || || || || || || || || || || || || || || || ||
QY 4002 AGTTTTGAAAAAAA 4015
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Db 14 AGTTTTGAAAAAAA 1
   || || || || || || || || || || || || || || || || || || || || ||

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RESULT 13

BE371943

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BE371943

BE371943.1

GI:9317215

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

601217728F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',

866 bp mRNA linear EST 21-JUL-2000

MRNA sequence.

BE371943

BE371943.1

GI:9317215

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 866)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM8748 row: h column: 07

High quality sequence stop: 639.

FEATURES	SOURCE
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3. The fourth column is labeled "SOURCE".	
4. The fifth column is labeled "FEATURES".	
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6. The seventh column is labeled "FEATURES".	
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/strain="CZECH II"
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/clone_image="3586614"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site.1: Salt;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
157 a 231 c 253 g 225 t
BASE COUNT
ORIGIN

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Query Match
Best Local Similarity 6.7%; Score 267; DB 10; Length 866;
Matches 333; Conservative 0; Mismatches 110; Indels
Pred. No. 7.4e-43;

[illegible]

2526 CCTACGTCAGTGCAGGGGATCCCGAGGGTCCATCCTCTCCACGCTGCTCTGCAGCC 2585

62 GCTATAGCGCAGTGGCCAGGGCATCCCCCAAGGCTCCAGCCTATCCACCCTGCTCTGCACTC 121

[illegible]

QY 2846 TCGGTTTGGTGGATGATTTCTTGTGTGGTGACACTCACTCACCCACGGGAAAAAGCTTCC 2705

Db
182 TACGTTTTTGATGACTTTCTGTTGGTGACGCTCACTTGGACCAAGCAAAAACCTTCC 241

QY 2706 TCAGGACCCCTGGTCCGAGGGTGTCCCTCAGTATGGCTGGTGGTGAACCTTCGGGAACACAG 2765

Db 242 TCAGCACCCCTGGTCCATGGCGTTCTCAGTAGTGGATGCATGATAAACTTGCAGAAAGACAG 301

QY 2766 TGGTGAACCTTCCCTGTAGAACACGAGGCCCTGGGTGGCAGGCCTTTTGTTCAGATGCCGG 2825

Db 302 TGGTGAACCTCCCTGTGGAGCCTGGTGCCTGGGGTGGTGCAGCTCCATACACAGTCCTG 361

2826 CCCAGGCCATTCCCTGGTGGCGCTGCTGCTGATACCCGGACCTCGAGGTGCAGA 2885

DB 362 CTCACCTGCCTGTTTCCCTTGGTGTGCTGCTGGACACTCAGACTTTGGAGGTCT 421

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[illegible]

RESULT 14
BE396925

LOCUS	BE396925	715 bp	mRNA	linear	EST 21-JUL-2000
DEFINITION	D1290610F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621050 5', mRNA sequence.				
ACCESSION	BE396925				
VERSION	BE396925.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 715)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: L12CM294 row: c column: 03 High quality sequence stop: 634.				

FEATURES

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/organism="Homo sapiens"
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/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/notes="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(6). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
119 a 164 c 266 g 166 t

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Query Match 6.3%; Score 252.2; DB 10; Length 715;
Best Local Similarity 93.9%; Pred. No. 6.3e-40;
Matches 307; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

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Db 372 AGGGTTGGCTGTGTTCGGCCGCGAGAGCACCGTCTCGGTGAGGAGATCTGGCCAAGTT 431

1687 CTGCAC^{TGGCTGATGAGTGTG}TACGTCGCGAGTCGCTCAGGTCCTTCTTT-TATGTCA 1745

Db 432 CCTGCACCTGGCTGATCAGTGTACCTGCTCGAGCTCCTCAGGCTTTCTTTTATATGTC 491

CGAGAGCAGCGTTTCATAAAGAACAAGGCTCTTTTCTTACCGGAAGAGTCTCTGGAGCAAGT 1805
1746
492
db

22	492	CGGAGACCAAGTTCATTTGAAATGAACAGGCCTCTTTTCTACCGAAGASTGTCTTGAGCAAGT	551
QY	1806	TGCAAGACACTTGGTAATCAGACAGCAACTTTGAAGAGAGGCTGCACCTGCGCCGACCT - CTTCCGDA	1864

Db 552 TGCAAGCATTTGGAAATCAGACAGCACTTGAAGAGGGTTGCACCTGGGGGACCTAGTCGGAA 611

QY 1865 GCAGAGGTCAGGCAGCATCGGG--AAGCCAGGCCCGCCCTGCTGACTCCAGACTCCGCT 1922

D_b 612 GCAGAGGTCAGGCAGCATCGGGGAAGCCAGGCCCTGCCTGCTCAGCTCA---ACTCCG 668

QY
1923 TCATCCCAAGCTGACGGGCTGCGGC 1949

Db
669 TTATCCCCAAGCTGAAGGCTGCGGC 695

RESULT 15

AA311750
LOCUS EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA linear EST 19-APR-1997
DEFINITION sequence.
ACCESSION AA311750
VERSION AA311750.1 GI:1964077
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 409)

ADAMS, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-I., Marnaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A., He, W.W.,
, Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

7566098

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1. .409

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="ATCC (inhost):158964"

/db_xref="taxon:9606"

/cell_type="T-lymphocyte"

/clone_lib="Jurkat T-cells VI"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT 65 a 120 c 133 g 86 t 5 others

ORIGIN

Query Match 6.2%; Score 249.6; DB 9; Length 409;

Best Local Similarity 97.7%; Pred. No. 1.8e-39;

Matches 252; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2649 GTTGGTGGATGATTTCTTTGGTGACACCTCACCTCACCCACGGGAAACCTTCCTCA 2708

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1 GTTTGGTGGATGATTTCTTTGGTGACACCTCACCTCACCCACGGGAAACCTTCCTCA 60

QY 2709 GGACCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGGTGAACCTTGGCGAAGACAGTGG 2768

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61 GGACCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGGTGAACCTTGGCGAAGACAGTGG 120

QY 2769 TGAACCTCCCTGTAGAGACGAGCGCCCTGGTGGCAGCGCTTTTGTTCAGATCCCGGCC 2828

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 21:56:28 ; Search time 14222 Seconds
(without alignments)
11549.160 Million cell updates/sec

Title: US-10-054-295-224
Perfect score: 4015
Sequence: 1 GCAGCGCGCGTCGCGCGC.....TTTTTCAGTTTGTGAAAAAAA 4015

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_da.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_hgt_hum.*
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- 32: em_hgt_other.*
- 33: em_hgt_mus.*
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- 35: em_hgt_rod.*
- 36: em_hgt_mam.*
- 37: em_hgt_vrt.*
- 38: em_sy.*
- 39: em_hgtgo_hum.*
- 40: em_hgtgo_mus.*
- 41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4015	100.0	4015	6	AR104587	AR104587 Sequence
2	4015	100.0	4015	6	AR175848	AR175848 Sequence
3	4015	100.0	4015	6	AR182221	AR182221 Sequence
4	4015	100.0	4015	6	AR224455	AR224455 Sequence
5	4015	100.0	4015	6	AR226390	AR226390 Sequence
6	4015	100.0	4015	6	AR243328	AR243328 Sequence
7	4015	100.0	4015	6	AR263555	AR263555 Sequence
8	4015	100.0	4015	6	AR265996	AR265996 Sequence
9	4015	100.0	4015	6	AX019310	AX019310 Sequence
10	4015	100.0	4015	6	AX133979	AX133979 Sequence
11	4015	100.0	4015	6	AX552695	AX552695 Sequence
12	4015	100.0	4015	6	BD011044	BD011044 Human tel
13	4015	100.0	4015	6	BD015832	BD015832 Quantitat
14	4015	100.0	4015	6	BD082985	BD082985 Method fo
15	4015	100.0	4015	6	BD131727	BD131727 Method fo
16	4015	100.0	4015	6	E36793	E36793 Human telom
17	4015	100.0	4015	9	AF015950	AF015950 Homo sapi
18	4015	100.0	4042	6	AX001446	AX001446 Sequence
19	4015	100.0	4042	6	AX003121	AX003121 Sequence
20	4015	100.0	4042	6	BD136185	BD136185 Human tel
21	4015	100.0	4070	6	AX391846	AX391846 Sequence
22	4008.6	99.8	4037	6	BD011070	BD011070 Human tel
23	4008.6	99.8	4037	6	E36819	E36819 Human telom
24	4002	99.7	4027	9	AF018167	AF018167 Homo sapi
25	3849.2	95.9	4029	6	AR104586	AR104586 Sequence
26	3849.2	95.9	4029	6	AR175847	AR175847 Sequence
27	3849.2	95.9	4029	6	BD011069	BD011069 Human tel
28	3849.2	95.9	4029	6	E36818	E36818 Human telom
29	3641	90.7	3855	6	AR243330	AR243330 Sequence
30	3641	90.7	3855	6	BD011046	BD011046 Human tel
31	3641	90.7	3855	6	E36795	E36795 Human telom
32	3440.2	85.7	8960	12	AF043739	AF043739 Synthetic
33	3400	84.7	13766	6	AX553919	AX553919 Sequence
34	3399	84.7	3399	6	AX481414	AX481414 Sequence
35	3396	84.6	3396	6	BD091553	BD091553 Adult bon
36	3396	84.6	3396	6	BD094749	BD094749 The cell
37	3396	84.6	3396	6	BD096291	BD096291 Cells cap
38	3388	84.4	8742	6	AX553924	AX553924 Sequence
39	3011	75.0	3210	9	AB085628	AB085628 Homo sapi
40	2637	65.7	3028	9	AB086379	AB086379 Homo sapi
41	2555	63.6	2992	9	AB086950	AB086950 Homo sapi
42	2335.4	58.2	2337	6	E22277	E22277 Higher anim
43	1961.4	48.9	2175	6	E22279	E22279 Higher anim
44	1960.4	48.8	2176	6	AR243329	AR243329 Sequence
45	1960.4	48.8	2176	6	BD011045	BD011045 Human tel

ALIGNMENTS

RESULT 1

AR104587

LOCUS

DEFINITION

AR104587

SEQUENCE

4015 bp

Sequence 224 from patent US 6093809.

Accession

AR104587

Version

AR104587.1

GI:12817295

Keywords

Unknown.

Source

Unknown.

Organism

Unclassified.

Reference

1 (bases 1 to 4015)

Cech,T.R. and Lingner,J.

Telomerase

Patent: US 6093809-A 224 25-JUL-2000;

Location/Qualifiers

linear PAT 14-FEB-2001

source	1. .4015	/organism="unknown"		
BASE COUNT	663 a	1363 c 1275 g 714 t		
ORIGIN				
Query Match 100.0%; Score 4015; DB 6; Length 4015;				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GCAGCGTGGCTCCTGCTGGCGACGCTGGGAAGCCCTGCCGCCGGCCACCCCGCGATGCC 60		
Db	1	GCAGCGTGGCTCCTGCTGGCGACGCTGGGAAGCCCTGSCCCCGGCCACCCCGCGATGCC 60		
Qy	61	CGCGGCTCCCGGCTGCCGAGCCGTGGCTCCCTGCTGGGCGAGCCACTACCCGCGAGTGCT 120		
Db	61	CGCGGCTCCCGGCTGCCGAGCCGTGGCTCCCTGCTGGCGAGCCACTACCCGCGAGTGCT 120		
Qy	121	GCCCTTGGCCACGTTCTGTGGCGGCCCTGGGCCCCAGGGCTGGCGGCTGGTGGCGAGCCGGG 180		
Db	121	GCCCTTGGCCACGTTCTGTGGCGGCCCTGGGCCCCAGGGCTGGCGGCTGGTGGCGAGCCGGG 180		
Qy	181	GGACCCGGCGGCTTTCCGCGCGCTGTGTGGCCACAGTGGCTGGTGTGCTGCTGCCCTGGGACGC 240		
Db	181	GGACCCGGCGGCTTTCCGCGCGCTGTGTGGCCACAGTGGCTGGTGTGCTGCTGCCCTGGGACGC 240		
Qy	241	ACGGCCCGCCCCCGCCGCCCTCCTTTCCGGCCAGGTGTCTGCTGAAGAGCTGTGTGGC 300		
Db	241	ACGGCCCGCCCCCGCCGCCCTCCTTTCCGGCCAGGTGTCTGCTGAAGAGCTGTGTGGC 300		
Qy	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGGCCGAAGAAGCTGTGGCGCTTTCGGCTTTCGC 360		
Db	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGGCCGAAGAAGCTGTGGCGCTTTCGGCTTTCGC 360		
Qy	361	GCTGCTGGACGGGCGCGCGGGGGCCCCCGAGGGCTTACCAACACAGCTGCGCAGCTA 420		
Db	361	GCTGCTGGACGGGCGCGCGGGGGCCCCCGAGGGCTTACCAACACAGCTGCGCAGCTA 420		
Qy	421	CGTGCCCAACACAGCTGACCGACGACCTGCGGGGAGCGGGCGCTGGGGGCTGCTGCTGC 480		
Db	421	CGTGCCCAACACAGCTGACCGACGACCTGCGGGGAGCGGGCGCTGGGGGCTGCTGCTGC 480		
Qy	481	CCGCGTGGGGGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT 540		
Db	481	CCGCGTGGGGGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT 540		
Qy	541	GGCTCCAGCTGGGCTTACAGGTGTGCGGGGCCCGCGCTGTACAGCTGGCGCTGCCAC 600		
Db	541	GGCTCCAGCTGGGCTTACAGGTGTGCGGGGCCCGCGCTGTACAGCTGGCGCTGCCAC 600		
Qy	601	TCAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAACGGGC 660		
Db	601	TCAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAACGGGC 660		
Qy	661	CTGGAACCATAGCCTCAGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCGGGTGGCGAG 720		
Db	661	CTGGAACCATAGCCTCAGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCGGGTGGCGAG 720		
Qy	721	GAGCGGGGGGAGTGCCGAGCGAAGCTGTGCGGTTGCCCAAGAGGCCCAAGCGCTGGCGC 780		
Db	721	GAGCGGGGGGAGTGCCGAGCGAAGCTGTGCGGTTGCCCAAGAGGCCCAAGCGCTGGCGC 780		
Qy	781	TGCCCCGTAGCCGAGCGGACGCCGTGGGAGGGGTCTGGGCCCAACCCGGCGCAGGAC 840		
Db	781	TGCCCCGTAGCCGAGCGGACGCCGTGGGAGGGGTCTGGGCCCAACCCGGCGCAGGAC 840		
Qy	841	CGCTGGACCGAGTGACCGTGGTTCCTGTGTGGTGTACCTGCCAGACCCCGCAAGAACG 900		
Db	841	CGCTGGACCGAGTGACCGTGGTTCCTGTGTGGTGTACCTGCCAGACCCCGCAAGAACG 900		
Qy	901	CACCTCTTTGGAGGTGGCTCTCTGCGACCGGCGCACTCCCAACCCATCGGTGGGCCGCCA 960		
Db	901	CACCTCTTTGGAGGTGGCTCTCTGCGACCGGCGCACTCCCAACCCATCGGTGGGCCGCCA 960		

[illegible]

QY	2041	CAGCGTGCCTCAACTACAGAGGGGGCGCGCGCCCGCGGCTCCTGGGGGCCCTCTGTGCTGGG	2100
DB	2041	CAGCGTGCCTCAACTACAGAGGGGGCGCGCGCCCGCGGCTCCTGGGGGCCCTCTGTGCTGGG	2100
QY	2101	CCTGGACGATATCCACAGAGGCGCTTGGCCACCTTTCGTGCTGCTGCTGTGGGGGCCCAGACCC	2160
DB	2101	CCTGGACGATATCCACAGAGGCGCTTGGCCACCTTTCGTGCTGCTGCTGTGGGGGCCCAGACCC	2160
QY	2161	GCCGCCCTGAGCTGTACTTTTCTCAAGGTGGATGTGAGGGGGCGCTAGCACACCATCCCCCA	2220
DB	2161	GCCGCCCTGAGCTGTACTTTTCTCAAGGTGGATGTGAGGGGGCGCTAGCACACCATCCCCCA	2220
QY	2221	GGACAGGCTCACGGAGGTCTATCGCCAGCATCATAAACCCAGAACGCTACTGCGTGGC	2280
DB	2221	GGACAGGCTCACGGAGGTCTATCGCCAGCATCATAAACCCAGAACGCTACTGCGTGGC	2280
QY	2281	TCGGTATGCCGTGTCCAGAGGGCCGCCATGGCAGCTCCGCAAGGCCCTTCAGAGCCCA	2340
DB	2281	TCGGTATGCCGTGTCCAGAGGGCCGCCATGGCAGCTCCGCAAGGCCCTTCAGAGCCCA	2340
QY	2341	CGTCTCTACCTTGACACAGACCTCCAGCCGCTACATGCGACAGTTTGGTGCTCACCTGCAGGA	2400
DB	2341	CGTCTCTACCTTGACACAGACCTCCAGCCGCTACATGCGACAGTTTGGTGCTCACCTGCAGGA	2400
QY	2401	GACCAGCCCGCTGAGGGATCGCTGTCTATCGAGCAGAGTCTCTCCTGAATGAGGCCAG	2460
DB	2401	GACCAGCCCGCTGAGGGATCGCTGTCTATCGAGCAGAGTCTCTCCTGAATGAGGCCAG	2460
QY	2461	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCACACGCGCTGGCATCAGGGG	2520
DB	2461	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCACACGCGCTGGCATCAGGGG	2520
QY	2521	CAAGTCTCTAGCTCCAGTCCAGGCCAGGGATCCCGCAGAGGCTCCATCTCTCCACGCTGCTCTG	2580
DB	2521	CAAGTCTCTAGCTCCAGTCCAGGCCAGGGATCCCGCAGAGGCTCCATCTCTCCACGCTGCTCTG	2580
QY	2581	CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTCGCGGGATTCGGCGGACCGGCT	2640
DB	2581	CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTCGCGGGATTCGGCGGACCGGCT	2640
QY	2641	GCTCCTCGTTCGTTGGTGATGATTCTTGTGTTGGTGACACCTCACCTCACCCACGCGAAAC	2700
DB	2641	GCTCCTCGTTCGTTGGTGATGATTCTTGTGTTGGTGACACCTCACCTCACCCACGCGAAAC	2700
QY	2701	CTTCCTCAGGACCTTGCTCCGAGGTGCCCTGAGTATGCGTGGGTGGACGCGCTTTGTTGAGAT	2760
DB	2701	CTTCCTCAGGACCTTGCTCCGAGGTGCCCTGAGTATGCGTGGGTGGACGCGCTTTGTTGAGAT	2760
QY	2761	GACAGTGGTGAATTCCTCTAGAACAGAGGCCCTGGGTGGACGCGCTTTGTTGTCAGAT	2820
DB	2761	GACAGTGGTGAATTCCTCTAGAACAGAGGCCCTGGGTGGACGCGCTTTGTTGTCAGAT	2820
QY	2821	GCCGGCCACGGCCCTATTCCTCTGGTGGCGGCTGCTGGATACCCGGACCCCTGGAGGT	2880
DB	2821	GCCGGCCACGGCCCTATTCCTCTGGTGGCGGCTGCTGGATACCCGGACCCCTGGAGGT	2880
QY	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
DB	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGGAGGAACATGCTGTCGCAAACTCTTTGGGTCTTTGGGCTGAAGTG	3000
DB	2941	CGGCTTCAAGGCTGGGAGGAACATGCTGTCGCAAACTCTTTGGGTCTTTGGGCTGAAGTG	3000
QY	3001	TCACAGCCTGTTCTTGATTTGACAGTGAACAGCCTCCAGACCGTGTGCACCAACATCTA	3060
DB	3001	TCACAGCCTGTTCTTGATTTGACAGTGAACAGCCTCCAGACCGTGTGCACCAACATCTA	3060
QY	3061	CAAGATCTCTCTGCTGACGCGTACAGTTTTCACGATGTGTGCTCGAGCTCCATTCTCA	3120
DB	3061	CAAGATCTCTCTGCTGACGCGTACAGTTTTCACGATGTGTGCTCGAGCTCCATTCTCA	3120
QY	3121	TCAGCAAGTTTGAAGAACCCTACATTTTTCCTGCGGCTCATCTCTGACACGCGCTCCCT	3180

[illegible]

[illegible]

Qy	2041	CAGCGTCTCAACTACAGAGGGGGGGGGCGCCCGCCCGGCTCCTGGGGGCCCTCTGTGCTGGG	2100
Db	2041	CAGCGTCTCAACTACAGAGGGGGGGGGCGCCCGCCCGGCTCCTGGGGGCCCTCTGTGCTGGG	2100
Qy	2101	CTGTGGAGATATCCACAGGGCCTTGGCGCACTTCGTGCTGCTGCTGGGGCCCGAGNCCC	2160
Db	2101	CTGTGGAGATATCCACAGGGCCTTGGCGCACTTCGTGCTGCTGCTGGGGCCCGAGNCCC	2160
Qy	2161	GGCGCTTGAGCTGTACTTTTCAAGGTGGATGTGACGGGGCGCTAGACACCACTCCCCCA	2220
Db	2161	GGCGCTTGAGCTGTACTTTTCAAGGTGGATGTGACGGGGCGCTAGACACCACTCCCCCA	2220
Qy	2221	GGACAGGCTCAGGGAGTCTATCGCGCAGCATCATCAACCCCAAGACAGTACTGCTGGG	2280
Db	2221	GGACAGGCTCAGGGAGTCTATCGCGCAGCATCATCAACCCCAAGACAGTACTGCTGGG	2280
Qy	2281	TCGGTATGCCGTTCAGAAAGGCGGCCATGGCAGCTCCGCAAGGCCCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCCGTTCAGAAAGGCGGCCATGGCAGCTCCGCAAGGCCCTTCAAGAGCCA	2340
Qy	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGAGGA	2400
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGAGGA	2400
Qy	2401	GACCAGCCGCTGAGGGATCCGCTGCTCATCGACGAGAGTCTCTCCCTGAATGAGGCCAG	2460
Db	2401	GACCAGCCGCTGAGGGATCCGCTGCTCATCGACGAGAGTCTCTCCCTGAATGAGGCCAG	2460
Qy	2461	CAGTGGGCTCTTGACAGCTTCTTACGCTTTCATGTGCGACACCGCGCTGGGCATCAGGGG	2520
Db	2461	CAGTGGGCTCTTGACAGCTTCTTACGCTTTCATGTGCGACACCGCGCTGGGCATCAGGGG	2520
Qy	2521	CAAGTCTCATGCTCAGTGCAGGGATCCCGCAGGGGTCCATCCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTCATGCTCAGTGCAGGGATCCCGCAGGGGTCCATCCTCTCCACGCTGCTCTG	2580
Qy	2581	CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGACCGGGCT	2640
Db	2581	CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGACCGGGCT	2640
Qy	2641	GCTCCTGCGTTTGGTGGATGATTCTTGTGTGGTGACACCTCACCTCACCCACCGGAAAC	2700
Db	2641	GCTCCTGCGTTTGGTGGATGATTCTTGTGTGGTGACACCTCACCTCACCCACCGGAAAC	2700
Qy	2701	CTTCTCAGACCCCTGTGCTCGAGGTGCTCAGTATGCGTGGTGAACTTGCGGAA	2760
Db	2701	CTTCTCAGACCCCTGTGCTCGAGGTGCTCAGTATGCGTGGTGAACTTGCGGAA	2760
Qy	2761	GACAGTGGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAGCGCTTTGTCAGAT	2820
Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAGCGCTTTGTCAGAT	2820
Qy	2821	GGCGGCCACGGGCTATTCCCTCTGGTGGCGCCCTGCTGCTGGATACCCGGACCCCTGGAGGT	2880
Db	2821	GGCGGCCACGGGCTATTCCCTCTGGTGGCGCCCTGCTGCTGGATACCCGGACCCCTGGAGGT	2880
Qy	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Qy	2941	CGGCTTCAAGCTGGGAGAAACATGCGTCGCAAACTCTTTGGGCTCTTGGCGCTGAAGTG	3000
Db	2941	CGGCTTCAAGCTGGGAGAAACATGCGTCGCAAACTCTTTGGGCTCTTGGCGCTGAAGTG	3000
Qy	3001	TCACAGCCTGTTTCTGGATTTCAGGTTGAACAGCCTCCAGACGCTGTCAGCCTCCATCTCA	3060
Db	3001	TCACAGCCTGTTTCTGGATTTCAGGTTGAACAGCCTCCAGACGCTGTCAGCCTCCATCTCA	3060
Qy	3061	CAAGATCCTCTGCTGCAGCGGTACAGTTTTCAGGTTTTCAGGATGTCAGCTCCCATTTCA	3120
Db	3061	CAAGATCCTCTGCTGCAGCGGTACAGTTTTCAGGTTTTCAGGATGTCAGCTCCCATTTCA	3120

Qy	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGGTCATCTCTGACACGGCCCTCCCT	3181
Db	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGGTCATCTCTGACACGGCCCTCCCT	3180
Qy	3181	CTGCTACTCCATCCTGAAGCCAGACGAGGATGTGCTGGGGGCCAAGGGCGCGC	3240
Db	3181	CTGCTACTCCATCCTGAAGCCAGACGAGGATGTGCTGGGGGCCAAGGGCGCGC	3240
Qy	3241	CGGCCCCCTTGCCCTCCGAGGCCGTGACGTGGCTGTGCGACCAAGCATTTCTGTCTCAAGCT	3300
Db	3241	CGGCCCCCTTGCCCTCCGAGGCCGTGACGTGGCTGTGCGACCAAGCATTTCTGTCTCAAGCT	3300
Qy	3301	GACTCGACACGGTGTCACTACGTGCGACCTCTGGGTCTACTCAGGACAGCCACAGCGCA	3360
Db	3301	GACTCGACACGGTGTCACTACGTGCGACCTCTGGGTCTACTCAGGACAGCCACAGCGCA	3360
Qy	3361	GCTCAGTCGGGAAGCTCCCGGGGACGCTGACTGCTGCTGGAGCCCGCAGCCACCCGGC	3420
Db	3361	GCTCAGTCGGGAAGCTCCCGGGGACGCTGACTGCTGCTGGAGCCCGCAGCCACCCGGC	3420
Qy	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGGA	3480
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGGA	3480
Qy	3481	GAGCAGACACAGCAGCCCTGTACGCCGGGCTCTACTCCACAGGAGGAGGGGCGGCC	3540
Db	3481	GAGCAGACACAGCAGCCCTGTACGCCGGGCTCTACTCCACAGGAGGAGGGGCGGCC	3540
Qy	3541	CACACCCAGGCCCGCCAGCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTGTTGGCCGAGGGCTG	3600
Db	3541	CACACCCAGGCCCGCCAGCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTGTTGGCCGAGGGCTG	3600
Qy	3601	CATGTCGGGCTGAAGGTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCCAAGGCT	3660
Db	3601	CATGTCGGGCTGAAGGTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCCAAGGCT	3660
Qy	3661	GAGTGTCCAGCACACCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGCACACCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
Qy	3721	GGGCCAGCTTTTCTCACCAGGACCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCTCACCAGGACCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
Qy	3781	CCAGATTCGCCATTGTTACACCCCTCGCCCTCGCCCTCTTGGCTTCCACCCCAACATCC	3840
Db	3781	CCAGATTCGCCATTGTTACACCCCTCGCCCTCGCCCTCTTGGCTTCCACCCCAACATCC	3840
Qy	3841	AGGTGGAGACCTTGAGAGGACCTGGAGCTCTGGGAATTTGAGTGTACCAAAAGTGTG	3900
Db	3841	AGGTGGAGACCTTGAGAGGACCTGGAGCTCTGGGAATTTGAGTGTACCAAAAGTGTG	3900
Qy	3901	CCCTGTACACAGGCGAGACCTCGACCTGGATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960
Db	3901	CCCTGTGTACACAGGCGAGACCTCGACCTGGATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960
Qy	3961	GAGTGTCTGGGAGTAAATACATGATATAGTATATATAGTATATATAGTATATAGTATATAGT	4015
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LOCUS	AR224455	4015 bp	DNA linear PAT 26-SEP-2002
DEFINITION	Sequence 1 from patent US 6440735.		
ACCESSION	AR224455		
VERSION	AR224455.1	GI:23333293	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 4015)		
AUTHORS	Gaeta, F.C.A.		

TITLE Dendritic cell vaccine containing telomerase reverse transcriptase
for the treatment of cancer
JOURNAL Patent: US 6440735-A 1 27-AUG-2002;
FEATURES Location/Qualifiers
source 1. .4015
BASE COUNT 563 a 1363 c 1275 g 714 t
ORIGIN

Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 60
DB 1 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 60
QY 61 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 120
DB 61 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 120
QY 121 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 180
DB 121 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 180
QY 181 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 240
DB 181 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 240
QY 241 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 300
DB 241 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 300
QY 301 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 360
DB 301 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 360
QY 361 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 420
DB 361 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 420
QY 421 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 480
DB 421 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 480
QY 481 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 540
DB 481 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 540
QY 541 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 600
DB 541 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 600
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DB 601 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 660
QY 661 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 720
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QY 721 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 780
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QY 841 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 900
DB 841 GCAGCGGTGCTCTGCTGGCAGTGGGAGCCCTGGCCCGCCGACCCCGCCGATGCC 900

QY 901 CACCTCTTTGGAGGTGCGCTCTCTGGCAGCGGCCACTCCACCCATCCGTGGCGCGCA 960
DB 901 CACCTCTTTGGAGGTGCGCTCTCTGGCAGCGGCCACTCCACCCATCCGTGGCGCGCA 960
QY 961 GCACACACGCGGCGCCCGCCATCCACATCGCGGCGCACACGTCCTCGGACACGCTTGTC 1020
DB 961 GCACACACGCGGCGCCCGCCATCCACATCGCGGCGCACACGTCCTCGGACACGCTTGTC 1020
QY 1021 CCCGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGCAGTGGC 1080
DB 1021 CCCGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGCAGTGGC 1080
QY 1081 GCGCTCTCTCTACTCAGCTCTCTGAGGCGCAGCTGACTGGGCTCGAGGCTCTGGA 1140
DB 1081 GCGCTCTCTCTACTCAGCTCTCTGAGGCGCAGCTGACTGGGCTCGAGGCTCTGGA 1140
QY 1141 GACCATCTTCTGGGTTTCAGGCGCTTGGATGCCAGGACTCCCGCAGGTTGCCCGCT 1200
DB 1141 GACCATCTTCTGGGTTTCAGGCGCTTGGATGCCAGGACTCCCGCAGGTTGCCCGCT 1200
QY 1201 GCGCCAGCGCTACTGCAAAATCGCGCCCTGTCTTCTGAGCTGCTTTGGAAACACGCGCA 1260
DB 1201 GCGCCAGCGCTACTGCAAAATCGCGCCCTGTCTTCTGAGCTGCTTTGGAAACACGCGCA 1260
QY 1261 GTGCGCTTACGGGCTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCAGC 1320
DB 1261 GTGCGCTTACGGGCTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCAGC 1320
QY 1321 AGCGGTGCTGTGTCGCGGAGAGCCCGCAGGCTCTGTGGCGGCGCCCGAGGAGGAGGA 1380
DB 1321 AGCGGTGCTGTGTCGCGGAGAGCCCGCAGGCTCTGTGGCGGCGCCCGAGGAGGAGGA 1380
QY 1381 CACAGACCCCGCTGCGCTGCTGCGGCTGCTCCCGCAGCAGCAGCAGCAGCAGTGTGA 1440
DB 1381 CACAGACCCCGCTGCGCTGCTGCGGCTGCTCCCGCAGCAGCAGCAGCAGCAGTGTGA 1440
QY 1441 CGGCTTCTGTCGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGG 1500
DB 1441 CGGCTTCTGTCGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGG 1500
QY 1501 CACAGAACCGCGCTTCTCAGGAACACCAAGAGTTCTATCTCCCTGGGAGAGCATGCCAA 1560
DB 1501 CACAGAACCGCGCTTCTCAGGAACACCAAGAGTTCTATCTCCCTGGGAGAGCATGCCAA 1560
QY 1561 GCTCTCGCTGCGAGGCTGACGTGGAAGATGAGCGTGGGAGTGGCTTGGCTGGCGAG 1620
DB 1561 GCTCTCGCTGCGAGGCTGACGTGGAAGATGAGCGTGGGAGTGGCTTGGCTGGCGAG 1620
QY 1621 GAGCCAGGCGTGGCTGCTGCGCGCGCAGAGCAGCAGTGGCTGAGGAGATCTGGC 1680
DB 1621 GAGCCAGGCGTGGCTGCTGCGCGCGCAGAGCAGCAGTGGCTGAGGAGATCTGGC 1680
QY 1681 CAAAGTTCTGCTGCTGATGATGTACGTGCTGCGAGCTGCTCAGGCTCTTTCTTTA 1740
DB 1681 CAAAGTTCTGCTGCTGATGATGTACGTGCTGCGAGCTGCTCAGGCTCTTTCTTTA 1740
QY 1741 TGTCAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
DB 1741 TGTCAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
QY 1801 CAAAGTTGCAAGCATTTGGAATCAGACAGTGTGAAGAGGTCAGCTGGGAGTGTCT 1860
DB 1801 CAAAGTTGCAAGCATTTGGAATCAGACAGTGTGAAGAGGTCAGCTGGGAGTGTCT 1860
QY 1861 GGAAGCAGAGGTGAGCAGCATCGGAAGCCAGGCGCGCCCTGCTCAGCTCAGACTCCG 1920
DB 1861 GGAAGCAGAGGTGAGCAGCATCGGAAGCCAGGCGCGCCCTGCTCAGCTCAGACTCCG 1920
QY 1921 CTTTCATCCCAACGCTGACGCGGCTGGGCGATGTGAACATGACTACGTCTGGGAGC 1980
DB 1921 CTTTCATCCCAACGCTGACGCGGCTGGGCGATGTGAACATGACTACGTCTGGGAGC 1980
QY 1981 CAGAACGTTCCGCGAGAGAAAGGCGCGAGCTCTCACCTCGAGGCTGAAGCAGCTGTT 2040

[illegible]

Db	3061	CAAGATCCTCTCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGAGCTCCCATTTTCA	3120
QY	3121	TCAGCAAGTTTGGGAAGAACCCACATTTTTCCTCGGGTGCATCTCTGACAGGGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGGAAGAACCCACATTTTTCCTCGGGTGCATCTCTGACAGGGCTCCCT	3180
QY	3181	CTGCTACTCCATCTCTGAAGCCAAAGAACGCAGGATGTCTGTGGGGCCAAAGGGCGCGC	3240
Db	3181	CTGCTACTCCATCTCTGAAGCCAAAGAACGCAGGATGTCTGTGGGGCCAAAGGGCGCGC	3240
QY	3241	CGGGCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT	3300
Db	3241	CGGGCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT	3300
QY	3301	GACTCGACACCGTGTCACTTACGTGCCACTCTCGGGTCTACTCAGGACAGCCACAGACGA	3360
Db	3301	GACTCGACACCGTGTCACTTACGTGGCCACTCTGGGTCTACTCAGGACAGCCACAGACGA	3360
QY	3361	GCTGAGTCGGAAAGTCCCGGGAGCAGGCTGACTGCCCTGGAGGCCGACGCAACCCGGC	3420
Db	3361	GCTGAGTCGGAAAGTCCCGGGAGCAGGCTGACTGCCCTGGAGGCCGACGCAACCCGGC	3420
QY	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGAGCATGTATGGCCACCCGCCACAGCCAGCCGA	3480
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGAGCATGTATGGCCACCCGCCACAGCCAGCCGA	3480
QY	3481	GAGCAGACACCAAGCAGCCCTCTCAGCCGGGCTCTACTCTCCAGGGAGGAGGGCGGCC	3540
Db	3481	GAGCAGACACCAAGCAGCCCTCTCAGCCGGGCTCTACTCTCCAGGGAGGAGGGCGGCC	3540
QY	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGGCCGAGGCCTG	3600
Db	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGGCCGAGGCCTG	3600
QY	3601	CATGTCGGCTTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCACGCCAAGGCT	3660
Db	3601	CATGTCGGCTTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCACGCCAAGGCT	3660
QY	3661	GAGTGTCCAGCACACTTCCGCTCTTCACTTCCACAGGCTGGCGCTGGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGCACACTTCCGCTCTTCACTTCCACAGGCTGGCGCTGGCTCCACCCCA	3720
QY	3721	GGGCCAGCTTTTCTCACAGGAGCCGGCTTCCACTCCACATAGGAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCTCACAGGAGCCGGCTTCCACTCCACATAGGAATAGTCCATCC	3780
QY	3781	CCAGATTGCCATTGTCTACCCCTCGCCCTGCCCTCTCTTGGCTTCCACCCCA	3840
Db	3781	CCAGATTGCCATTGTCTACCCCTCGCCCTGCCCTCTCTTGGCTTCCACCCCA	3840
QY	3841	AGGTGGAGACCTCAGAAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTTG	3900
Db	3841	AGGTGGAGACCTCAGAAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTTG	3900
QY	3901	CCCTGTATACAGGCGAGSACCTGCACCTGGATGGGGTCCCTCTGGGTCAAATTTGGGG	3960
Db	3901	CCCTGTATACAGGCGAGSACCTGCACCTGGATGGGGTCCCTCTGGGTCAAATTTGGGG	3960
QY	3961	GAGTGTCTCGGGAGTAAATACATGATATATAGTATTTTTCAGTTCGATTTTGA	4015
Db	3961	GAGTGTCTCGGGAGTAAATACATGATATATAGTATTTTTCAGTTCGATTTTGA	4015

RESULT 5

AR226390
F. O. G. H. C.

LOCUS
DEFINITION

ACCESSION
NUMBER

KEYWORDS

SOURCE
ORGAN

TABLE 2

RESULT 5

AR226390
FOGTS

LOCUS ARZ26390 4015 bp
DEFINITION Sequence 1 from patent US 6444650.
MRNA linear PAT 20-DEC-2002

ACCESSION	AR226390	
VERSION	AR226390 1	CT:27264005

VERSION
KEYWORDS

ORGANISM	SOURCE
Unknown.	Unknown.
Unknown	Unknown

UNCLASSIFIED;
Unclassified.

REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Antisense compositions for detecting and inhibiting telomerase
reverse transcriptase
JOURNAL Patent: US 644650-A 1 03-SEP-2002;
FEATURES Location/Qualifiers
source 1. 4015
BASE COUNT 663 a 1363 c 1275 g 714 t
ORIGIN
Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGGGCTGCGTCTGTCGCGACGTTGGGAAGCCCTGGCCCGCGCCACCCCGGATGCC 60
DB 1 GCAGGGCTGCGTCTGTCGCGACGTTGGGAAGCCCTGGCCCGCGCCACCCCGGATGCC 60
QY 61 GCGCGTCCCGCTGCCGAGCGGTGCGCTCCCTGTCGCGACGCACTACCGCGAGGTGCT 120
DB 61 GCGCGTCCCGCTGCCGAGCGGTGCGCTCCCTGTCGCGACGCACTACCGCGAGGTGCT 120
QY 121 GCGCGTGGCGACGTTGTCGCGCGCTGGGGCCCGAGGGCTGGGGCTGGTGCAGCGGG 180
DB 121 GCGCGTGGCGACGTTGTCGCGCGCTGGGGCCCGAGGGCTGGGGCTGGTGCAGCGGG 180
QY 181 GGACCCGCGGCTTTCGCGCGCTGTGGCGCCAGTGCCTGTGTGCGCTGGGAGCG 240
DB 181 GGACCCGCGGCTTTCGCGCGCTGTGGCGCCAGTGCCTGTGTGCGCTGGGAGCG 240
QY 241 AGGGCGCCCGCGCGCCCTCTCCGCGAGGTGCTGCTGCGTGAAGAGAGCTGGTGGC 300
DB 241 AGGGCGCCCGCGCGCCCTCTCCGCGAGGTGCTGCTGCGTGAAGAGAGCTGGTGGC 300
QY 301 CCGAGTGTGACAGAGCTGTGGAGCGCGCGGAGAACGTCGTGGCTTCGCGCTTCGC 360
DB 301 CCGAGTGTGACAGAGCTGTGGAGCGCGCGGAGAACGTCGTGGCTTCGCGCTTCGC 360
QY 361 GCTGCTGACGGGGCGCGGGGGCCCGCGAGGCTTACACACAGCGTGGCGAGCTA 420
DB 361 GCTGCTGACGGGGCGCGGGGGCCCGCGAGGCTTACACACAGCGTGGCGAGCTA 420
QY 421 CTTGCCCAACAGGTGACGACGCTACTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGC 480
DB 421 CTTGCCCAACAGGTGACGACGCTACTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGC 480
QY 481 CCGCGTGGCGGACGACGCTGCTGCTACCTGCTGCGACGCTGCGGCTCTTTGTGCTG 540
DB 481 CCGCGTGGCGGACGACGCTGCTGCTACCTGCTGCGACGCTGCGGCTCTTTGTGCTG 540
QY 541 GGCTCCAGCTGCGCTTACCAAGTGTGGGGCGCGCGCTGTACCAAGCTGCGGCTGCCAC 600
DB 541 GGCTCCAGCTGCGCTTACCAAGTGTGGGGCGCGCGCTGTACCAAGCTGCGGCTGCCAC 600
QY 601 TCAGGCGCGGGCCCGCCACAGCTAGTGGAGCCCGAAGGCTGTGGATGGGAACGGGC 660
DB 601 TCAGGCGCGGGCCCGCCACAGCTAGTGGAGCCCGAAGGCTGTGGATGGGAACGGGC 660
QY 661 CTGGAAACCATAGCTCAGGAGCGGGGTCCCGTGGGCTGCCAGCCCGGGTGGAG 720
DB 661 CTGGAAACCATAGCTCAGGAGCGGGGTCCCGTGGGCTGCCAGCCCGGGTGGAG 720
QY 721 GAGGGCGGGGCACTGGCCAGCGGAGTCTGCGCTGGCTGGCCAGAGCGCCAGCGTGGGC 780
DB 721 GAGGGCGGGGCACTGGCCAGCGGAGTCTGCGCTGGCTGGCCAGAGCGCCAGCGTGGGC 780
QY 781 TGGCCCTGAGCGGAGCGGACGCCGTTGGGAGAGGGTCTCTGGGCGCCCGGGGAGGAC 840
DB 781 TGGCCCTGAGCGGAGCGGACGCCGTTGGGAGAGGGTCTCTGGGCGCCCGGGGAGGAC 840
QY 841 GCGTGGACCGAGTACCGGTGTTCTGCTGTGTGTCACCTGCTGACACCGCGCGAAGAC 900

841 GCCTGGACCGAGTACCGGTGTTCTGTGTGTGTCTACCTTGCAGAGCCCGCCGAAAGC 900
QY 901 CACTCTTTTGGAGGGTGCCTCTGTGCGCGCCACTCCACCCACTCCGTGGCGCGCCA 960
DB 901 CACTCTTTTGGAGGGTGCCTCTGTGCGCGCCACTCCACCCACTCCGTGGCGCGCCA 960
QY 961 GCACACGCGGGCCCCCATTCCACATCGCGGCCACACAGTCCCTGGGACACGCTGTGC 1020
DB 961 GCACACGCGGGCCCCCATTCCACATCGCGGCCACACAGTCCCTGGGACACGCTGTGC 1020
QY 1021 CCGGGTGTACGCGAGACCAAGCACTTCTCTACTCTCTAGGGGACAAAGAGAGCTGGC 1080
DB 1021 CCGGGTGTACGCGAGACCAAGCACTTCTCTACTCTCTAGGGGACAAAGAGAGCTGGC 1080
QY 1081 GCCCTCTTCTACTCAAGCTCTGTAGGCCAGCCTGACTTGGGCTCGGAGGCTCGTGA 1140
DB 1081 GCCCTCTTCTACTCAAGCTCTGTAGGCCAGCCTGACTTGGGCTCGGAGGCTCGTGA 1140
QY 1141 GACCATCTTTTGGGTTCCAGGGCCTGGATGCGAGGACTCCCGCGAGTTGCCCGCCT 1200
DB 1141 GACCATCTTTTGGGTTCCAGGGCCTGGATGCGAGGACTCCCGCGAGTTGCCCGCCT 1200
QY 1201 GCCCGAGCGTACTGCAAAATGCGGCCCTGTTCTGAGCTGCTTGGGAACACAGCGCA 1260
DB 1201 GCCCGAGCGTACTGCAAAATGCGGCCCTGTTCTGAGCTGCTTGGGAACACAGCGCA 1260
QY 1261 GTGCCCCCTAGGGGTGCTCCTCAAGACGCTGCCCCCTCGAGCTCGGTGCTACCCGAC 1320
DB 1261 GTGCCCCCTAGGGGTGCTCCTCAAGACGCTGCCCCCTCGAGCTCGGTGCTACCCGAC 1320
QY 1321 AGCGGTGTCTGTGCGGAGAGAGCCCGAGGGCTCTGTGGCGCCCGCGAGGAGGA 1380
DB 1321 AGCGGTGTCTGTGCGGAGAGAGCCCGAGGGCTCTGTGGCGCCCGCGAGGAGGA 1380
QY 1381 CACAGACCCCGTGCCTGTGTGCTGCTGCTCCGCGACACAGAGCCCTGCGAGGTGA 1440
DB 1381 CACAGACCCCGTGCCTGTGTGCTGCTGCTCCGCGACACAGAGCCCTGCGAGGTGA 1440
QY 1441 CGGCTTCTGTGGGGCTGCTGCTGCGCGGGTGGTGGCCCGAGGCTCTGGGGCTCCAGCA 1500
DB 1441 CGGCTTCTGTGGGGCTGCTGCTGCGCGGGTGGTGGCCCGAGGCTCTGGGGCTCCAGCA 1500
QY 1501 CAACGAACGCGCTTCTCTCAGGAACACCAAGAGTTCATCTCCCTGGGAGCATGCAA 1560
DB 1501 CAACGAACGCGCTTCTCTCAGGAACACCAAGAGTTCATCTCCCTGGGAGCATGCAA 1560
QY 1561 GCTCTGCTGAGGAGCTGAGTGAAGATGAGCGTGGGACTGCGCTGGCTGCGCAG 1620
DB 1561 GCTCTGCTGAGGAGCTGAGTGAAGATGAGCGTGGGACTGCGCTGGCTGCGCAG 1620
QY 1621 GAGCCAGGGGTTGGTGTGTTCCGGCGCAGACACCGTGTGCTGAGGAGATCTGGC 1680
DB 1621 GAGCCAGGGGTTGGTGTGTTCCGGCGCAGACACCGTGTGCTGAGGAGATCTGGC 1680
QY 1681 CAAGTCTCTGACGTGGCTGATGAGTGTAGTGTGCTGAGCTGCTCAGGTCTTTCTTTA 1740
DB 1681 CAAGTCTCTGACGTGGCTGATGAGTGTAGTGTGCTGAGCTGCTCAGGTCTTTCTTTA 1740
QY 1741 TGTCAAGGAGACCAAGTTCAGGAAGACAGGCTCTTTTCTACCGGAGAGTGTGAG 1800
DB 1741 TGTCAAGGAGACCAAGTTCAGGAAGACAGGCTCTTTTCTACCGGAGAGTGTGAG 1800
QY 1801 CAAGTTGCAAGCATTTGAATTCAGACAGCTTGAAGAGGTTGAGCTGCGGGAGCTGTC 1860
DB 1801 CAAGTTGCAAGCATTTGAATTCAGACAGCTTGAAGAGGTTGAGCTGCGGGAGCTGTC 1860
QY 1861 GGAAGCAGAGTTCAGGAGAGCATCGGAAGCCAGGCGCCCTGCTGAGTCCAGACTCCG 1920
DB 1861 GGAAGCAGAGTTCAGGAGAGCATCGGAAGCCAGGCGCCCTGCTGAGTCCAGACTCCG 1920
QY 1921 CTTTCATCCCCAAGCCTGACGGCTGCGGCGGATTGTGAACATGACTACGTGTTGGGAGC 1980
DB 1921 CTTTCATCCCCAAGCCTGACGGCTGCGGCGGATTGTGAACATGACTACGTGTTGGGAGC 1980

[illegible]

Qy	1921	CTTCAATCCCAAGCCTGACGGGTGCGGCCGATTGTGAACATGAGCTACGTCGTGGGAGC	1980
Db	1921	CTTCAATCCCAAGCCTGACGGGTGCGGCCGATTGTGAACATGAGCTACGTCGTGGGAGC	1980
Qy	1981	CAGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCAACCTCAGGGTGAAAGCACTGTT	2040
Db	1981	CAGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCAACCTCAGGGTGAAAGCACTGTT	2040
Qy	2041	CAGCGTGCTCAACTACAGCGGGCGGGCGGCCCGCCGCTCTCTGGGCGCCTCTCTGCTGGG	2100
Db	2041	CAGCGTGCTCAACTACAGCGGGCGGGCGGCCCGCCGCTCTCTGGGCGCCTCTCTGCTGGG	2100
Qy	2101	CTGTGGAGGATATCCACAGGGCCTGGGCGCACTTCGTGTGCTGCTGTGGGGCCCCAGACCC	2160
Db	2101	CTGTGGAGGATATCCACAGGGCCTGGGCGCACTTCGTGTGCTGCTGTGGGGCCCCAGACCC	2160
Qy	2161	GGCGCCTGAGCTGTACTTTCCTCAAGGTGGATGTGACGGGGCGCTACGACACCATCCCCCA	2220
Db	2161	GGCGCCTGAGCTGTACTTTCCTCAAGGTGGATGTGACGGGGCGCTACGACACCATCCCCCA	2220
Qy	2221	GGACAGGCTCACGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACACGCTACTTCGTGCG	2280
Db	2221	GGACAGGCTCACGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACACGCTACTTCGTGCG	2280
Qy	2281	TCGGTATGCGGTGTTCCAGAAAGCGGCCATGGCGACGTCCGGAAGCCCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCGGTGTTCCAGAAAGCGGCCATGGCGACGTCCGGAAGCCCTTCAAGAGCCA	2340
Qy	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCCTGCAGGA	2400
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCCTGCAGGA	2400
Qy	2401	GACAGCCGCTGAGGGATCCGTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG	2460
Db	2401	GACAGCCGCTGAGGGATCCGTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG	2460
Qy	2461	CAGTGGCCTCTCGACGCTTCTTAGCTTCATGTGCCACAGCGGTGCGCATCAGGG	2520
Db	2461	CAGTGGCCTCTCTCGACGCTTCTTAGCTTCATGTGCCACAGCGGTGCGCATCAGGG	2520
Qy	2521	CAAGTCTCTAGTCCAGTGCCAGGGGATCCCGCAGGGTCCATCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTCTAGTCCAGTGCCAGGGGATCCCGCAGGGTCCATCTCTCCACGCTGCTCTG	2580
Qy	2581	CAGCCTGTGTAGCGGACATGAGAGAACAGCTGTTTGGGGGATTGGCGGGACGGGCT	2640
Db	2581	CAGCCTGTGTAGCGGACATGAGAGAACAGCTGTTTGGGGGATTGGCGGGACGGGCT	2640
Qy	2641	GCTCCTCGGTTTGGTGGATCATTTCTTGTTGGTGACACCTCACTCACCACCGGAAAC	2700
Db	2641	GCTCCTCGGTTTGGTGGATCATTTCTTGTTGGTGACACCTCACTCACCACCGGAAAC	2700
Qy	2701	CTTCTCTCAGGACCTGGTCCGAGGTGCCCTGAGTATGGCTGGGTGAACCTTGGCGAA	2760
Db	2701	CTTCTCTCAGGACCTGGTCCGAGGTGCCCTGAGTATGGCTGGGTGAACCTTGGCGAA	2760
Qy	2761	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Qy	2821	GGCGGCCACCGGCTATTTCCCTTGTTGGCGGCTGCTGCTGGATACCCGGACCCCTGGAGT	2880
Db	2821	GGCGGCCACCGGCTATTTCCCTTGTTGGCGGCTGCTGCTGGATACCCGGACCCCTGGAGT	2880
Qy	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
Qy	2941	CGGCTTCAAGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGCTCTTCGGCTGAAGTG	3000
Db	2941	CGGCTTCAAGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGCTCTTCGGCTGAAGTG	3000

QY	3001	TCACAGCCTGTTTCTCGATTTCGAGGTGAACAGCCTCCAGACGGTGTGCACACATCTA	3061
DB	3001	TCACAGCCTGTTTCTCGATTTCGAGGTGAACAGCCTCCAGACGGTGTGCACACATCTA	3060
QY	3061	CAAGATCCTCTGCTGCAGGGGTACAGGTTTCAGGCATGTGTGCTGCAGTCCCATTTCA	3120
DB	3061	CAAGATCCTCTGCTGCAGGGGTACAGGTTTCAGGCATGTGTGCTGCAGTCCCATTTCA	3120
QY	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCTCGCGCTCATCTCTGCACAGGGCTCCCT	3180
DB	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCTCGCGCTCATCTCTGCACAGGGCTCCCT	3180
QY	3181	CTGCTACTCCATCTCTGAAGCAAGACAGCAGGATGTGGTGGGGGCCAAGGGCGCGC	3240
DB	3181	CTGCTACTCCATCTCTGAAGCAAGACAGCAGGATGTGGTGGGGGCCAAGGGCGCGC	3240
QY	3241	CGGGCCTCTGGCCCTCCGAGGCCGTGCAGTGGCTGTGCACCAAGCATTCCTGCTCAAGCT	3300
DB	3241	CGGGCCTCTGGCCCTCCGAGGCCGTGCAGTGGCTGTGCACCAAGCATTCCTGCTCAAGCT	3300
QY	3301	GACTCGACACCGTGTCACTACGTGCCACTCTCTGGGTCATCTCAGGACAGCCACAGCGCA	3360
DB	3301	GACTCGACACCGTGTCACTACGTGCCACTCTCTGGGTCATCTCAGGACAGCCACAGCGCA	3360
QY	3361	GCTGAGTCGGAAAGCTCCCGGGAGCAGCTGACTGTGCCCTTGAGGCCGCGCAACCCGGC	3420
DB	3361	GCTGAGTCGGAAAGCTCCCGGGAGCAGCTGACTGTGCCCTTGAGGCCGCGCAACCCGGC	3420
QY	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGAGCTGATGGCCACCCGCCACAGCCAGGCCGA	3480
DB	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGAGCTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3481	GAGCAGACACCAAGCAGCCCTGTACGCCGGGCTCTAGTCCCAAGGAGGAGGGCGGCC	3540
DB	3481	GAGCAGACACCAAGCAGCCCTGTACGCCGGGCTCTAGTCCCAAGGAGGAGGGCGGCC	3540
QY	3541	CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTGAGTGTGGCCGAGGGCTG	3600
DB	3541	CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTGAGTGTGGCCGAGGGCTG	3600
QY	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGGCT	3660
DB	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3661	GAGTGTCCAGCACACCTGCCCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
DB	3661	GAGTGTCCAGCACACCTGCCCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
QY	3721	GGGCCAGCTTTTCTTCACAGGAGCCGGCTTCCACATCCCCACATAGGAATAGTCCATCC	3780
DB	3721	GGGCCAGCTTTTCTTCACAGGAGCCGGCTTCCACATCCCCACATAGGAATAGTCCATCC	3780
QY	3781	CCAGATTGGCCATTGTTTCAACCCCTCGGCCCTGCCCTCTTTGGCTTCCACCCCAATCC	3840
DB	3781	CCAGATTGGCCATTGTTTCAACCCCTCGGCCCTGCCCTCTTTGGCTTCCACCCCAATCC	3840
QY	3841	AGGTGGAGACCCCTGAGAAGGACCCCTGGAGCTCTGGGAAATTGAGATGACCAAGAGTGTG	3900
DB	3841	AGGTGGAGACCCCTGAGAAGGACCCCTGGAGCTCTGGGAAATTGAGATGACCAAGAGTGTG	3900
QY	3901	CCCTGTACACAGGGGAGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAAATGGGGG	3960
DB	3901	CCCTGTACACAGGGGAGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAAATGGGGG	3960
QY	3961	GAGGTGCTGTGGGAGTAAATPACTGAATATAGTATTTTCAGTTTTGAAAAAA	4015
DB	3961	GAGGTGCTGTGGGAGTAAATPACTGAATATAGTATTTTCAGTTTTGAAAAAA	4015

RESULT 7
AR263555
LOCUS
DEFINITI

AR263555 4015 bp DNA linear PAT 29-JAN-2003
Sequence 3 from patent US 6331399.

[illegible]

Db 1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGCTCAGACTCGG 1920
QY 1921 CTTTATCCCAAGCCTGACGGCTCGGCCGATTTGTGAACATGAGTACGTCGTGGAGC 1980
Db 1921 CTTTATCCCAAGCCTGACGGCTCGGCCGATTTGTGAACATGAGTACGTCGTGGAGC 1980
QY 1981 CAGAACGTTCCGCAGAGAAAAGAGGCGGAGCGTCTACCTCGAGGGTGAAGCACTGTT 2040
Db 1981 CAGAACGTTCCGCAGAGAAAAGAGGCGGAGCGTCTACCTCGAGGGTGAAGCACTGTT 2040
QY 2041 CAGCGTGTCAACTACGAGGCGGCGGCCGCCGCCCTCCCTGCGGCGCTCTGTCGTGG 2100
Db 2041 CAGCGTGTCAACTACGAGGCGGCGGCCGCCGCCCTCCCTGCGGCGCTCTGTCGTGG 2100
QY 2101 CTTGACGATATCCACAGGCGCTGCGCACCTTCCTGTCGTGTCGTGTCGTGTCGTGTC 2160
Db 2101 CTTGACGATATCCACAGGCGCTGCGCACCTTCCTGTCGTGTCGTGTCGTGTCGTGTC 2160
QY 2161 GCCGCTGAGCTGACTTTGTCAAGGTGATGTGACGGCGGTACGACACCATCCCCCA 2220
Db 2161 GCCGCTGAGCTGACTTTGTCAAGGTGATGTGACGGCGGTACGACACCATCCCCCA 2220
QY 2221 GGACAGGCTCAGCGAGGTCATGCCAGCATCATCAAAACCCAGAACACACTACTGCGTGG 2280
Db 2221 GGACAGGCTCAGCGAGGTCATGCCAGCATCATCAAAACCCAGAACACACTACTGCGTGG 2280
QY 2281 TCGGTATGCGGTGTCAGAGGCGGCCCATGGGCACGTCGCCAAGGCGTTCAAGAGCCA 2340
Db 2281 TCGGTATGCGGTGTCAGAGGCGGCCCATGGGCACGTCGCCAAGGCGTTCAAGAGCCA 2340
QY 2341 CGTCTCTACTTTCAGACACTCCAGCGGTACATGCGACAGTTCGTCGCTCAGGAGCA 2400
Db 2341 CGTCTCTACTTTCAGACACTCCAGCGGTACATGCGACAGTTCGTCGCTCAGGAGCA 2400
QY 2401 GACCAGCGCGCTGAGGAGTCCGCTGCTCATCAGCAGAGCTCCTCCTGAATGAGGCCAG 2460
Db 2401 GACCAGCGCGCTGAGGAGTCCGCTGCTCATCAGCAGAGCTCCTCCTGAATGAGGCCAG 2460
QY 2461 CAGTGGCTCTTCGACGCTCTCCTACGCTTCATGTCGCCACCGCGTCGCATCAGGGG 2520
Db 2461 CAGTGGCTCTTCGACGCTCTCCTACGCTTCATGTCGCCACCGCGTCGCATCAGGGG 2520
QY 2521 CAAGTCTACGTCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCCTCAGCGTGTCTG 2580
Db 2521 CAAGTCTACGTCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCCTCAGCGTGTCTG 2580
QY 2581 CAGCCTGTGCTACGGCGACATGAGAAAGCTGTTTGGGGGATTCGCGGGAGCGGGCT 2640
Db 2581 CAGCCTGTGCTACGGCGACATGAGAAAGCTGTTTGGGGGATTCGCGGGAGCGGGCT 2640
QY 2641 GCTCTGCGTTTGGTGGATGATTTCTTGTGTTGACACCTCACCTCACCCAGCGGAAAC 2700
Db 2641 GCTCTGCGTTTGGTGGATGATTTCTTGTGTTGACACCTCACCTCACCCAGCGGAAAC 2700
QY 2701 CTTCTCAGGACCTTGGTCCGAGGTGTCCTCAGTATGCTGCGTGGTGAATCGGGAA 2760
Db 2701 CTTCTCAGGACCTTGGTCCGAGGTGTCCTCAGTATGCTGCGTGGTGAATCGGGAA 2760
QY 2761 GACAGTGTGAACTTCCCTGTAGAAAGACGAGCGCTGGGTGGCAGCGCTTTTGTTCAGAT 2820
Db 2761 GACAGTGTGAACTTCCCTGTAGAAAGACGAGCGCTGGGTGGCAGCGCTTTTGTTCAGAT 2820
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QY 2941 CGGCTTCAAGGCTGGGAGGAACATGGTCGCAAACTCTTTGGGGCTTCGCGCTGAGTG 3000
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RESULT 8

AR265996

LOCUS

AR265996

4015 bp

DNA

linear

PAT 10-APR-2003

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LOCUS AX019310 4015 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9940221.
ACCESSION AX019310
VERSION AX019310.1 GI:10043297
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Dahm,M.W., Phelps,R.C. and Brockmeyer,C.
TITLE Method for quantitatively analyzing tumor cells in a body fluid and
test kits suit therefor
JOURNAL Patent: WO 9940221-A 10 12-AUG-1999;
DAHM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)
FEATURES
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BASE COUNT 663 a 1363 c 1275 g 714 t
ORIGIN
Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1981	CAGAAAGTTCCCGCAGAGAAAGAGGCGCGAGCTCTACCTTCAGGGTGAAGCACTGTT	2040
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QY	2461	CAGTGGCTCTTTCGAGCTTCTCAGCTTCATGTGCCACCGCGTGCATCAGGGG	2520
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VERSION	AX133979.1	GI:14139919		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Chang, S.Y. and Santini, C.D.			
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Qy	241	ACGGCGCCCCCGCGCCCTCTTCCGCCAGGTGCTTCCGCGAGGTGCTTGAAGGAGCTGGTGC	300	
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Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCGC	360	
Qy	361	GCTGCTGGACGGGGCGCGGGGGCCCCCGAGGCTTACACACCGGTCGCAGCTA	420	
Db	361	GCTGCTGGACGGGGCGCGGGGGCCCCCGAGGCTTACACACCGGTCGCAGCTA	420	
Qy	421	CCTGCCAACAGGTGACCGAGCAGCTCGGGGGAGCGGGGCTGGCTCTGCG	480	
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DEFINITION Sequence 1 from Patent WO02074948.
ACCESSION AX552695
VERSION AX552695.1 GI:25896697
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Denning,C., Clark,A.J. and Schiff,J.M.
AUTHORS Animal tissue with carbohydrate antigens compatible for human
TITLE transplantation
JOURNAL Patent: WO 02074948-A 1 26-SEP-2002;
Geron Corporation (US)
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LOCUS Human telomerase catalytic subunit.
DEFINITION BD011044
ACCESSION BD011044
VERSION BD011044.1 GI:18639417
KEYWORDS JP 2001081042-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morf,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 1 27-MAR-2001;
GERON CORP, UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 2001081042-A/1
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
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09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
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MORIN,
PI CALVIN B HARLEY, WILLIAM H ANDREWS
PC A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,
PC C07K5/10, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12, PC
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LOCUS			
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ACCESSION		BD015832	
VERSION		BD015832.1 GI:22556969	
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SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1. (bases 1 to 4015)	
JOURNAL		Chang, S.Y.P. and Santini, C.D.	
COMMENT		Quantitation of expression of hTERmRNA	
		Patent: JP 2001204483-A 1 31-JUL-2001;	
		F. HOFFMANN LA ROCHE AG	
		OS Homo sapiens (human)	
		PN JP 2001204483-A/1	
		PD 31-JUL-2001	
		PF 18-DEC-2000 JP 2000384268	
		PR 16-DEC-1999 US 09/465491	
		PI SHEN YUN PAI CHANG, CHRISTOPHER DAVID SANTINI	
		PC C12N15/09, C12Q1/48, C12Q1/68, C12N15/00	
		CC Quantitation of expression of hTERmRNA	
		FH Key Location/Qualifiers	
		FT source 1..4015 /organism='Homo sapiens (human)'	
FEATURES		Location/Qualifiers	
source		1..4015 /organism='Homo sapiens' /mol_type='genomic DNA'	

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Qy	901	CACCTCTTTGGAGGTGGCGCTCTCTGGCACGGCCACTCCACACCATCCGTTGGCCGCCCA	960
Db	901	CACCTCTTTGGAGGTGGCGCTCTCTGGCACGGCCACTCCACACCATCCGTTGGCCGCCCA	960
Qy	961	GCACGACGGGGCCCCCAATCCACATCGGGGCCACCAAGTCCCTTGGGACAGCCCTTGTCC	1020
Db	961	GCACGACGGGGCCCCCAATCCACATCGGGGCCACCAAGTCCCTTGGGACAGCCCTTGTCC	1020
Qy	1021	CCCGGTGTACGCCGAGACCAAGCACTCTCTTACTCTCTCAGCGCAAGGAGCAGCTGCG	1080
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTCTCTTACTCTCTCAGCGCAAGGAGCAGCTGCG	1080
Qy	1081	GGCCTCCTTCTACTCAGCTCTCTGAGGCCAGCGCTGACTGGCGCTGGAGGCTCTGTGA	1140
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Qy	1201	GGCCGAGCGCTACTTGGCAATCGGCCCTCTTCTTGAGGCTGTGTGGGAACCAACCGCCA	1260
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Qy	1261	GTGCCCCCTACGGGGTCTCCTCAAGACGACTTGCOCGCTGGAGTGCGGTCAOCCAGC	1320
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Qy	1381	CACAGACCCCGCTCGCCTGGTGCAGCTGTCTCGCCAGCACAGACCCCTGGCAGGTGTA	1440
Db	1381	CACAGACCCCGCTCGCCTGGTGCAGCTGTCTCGCCAGCACAGACCCCTGGCAGGTGTA	1440
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Qy	1561	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGCAG	1620
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Qy	1861	GGAGCAGAGGTCAGGCACCATTCGGGAGCCAGGCCCGCCCTGCTGAGCTCCAGACTCCG	1920
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[illegible]

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QY	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGGCCACCGCCACAGCCAGGCCGA	3480
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Job time : 14244 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 20:23:54 ; Search time 988 Seconds
(without alignments)
10969.882 Million cell updates/sec

Title: US-10-054-295-224

Perfect score: 4015

Sequence: 1 GCAGCGCTGCCGTCCTGCTGC.....TTTTCAGTTTGAAAAAA 4015

Scoring table: IDENTITY_NUC

Learning curve: $\text{learning_curve} = \text{learning_curve_roc}$
Gapop 10.0 ; Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

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Post-processing: Minimum Match 08

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4015	100.0	4015	20	AAZ30154	cDNA encoding a hu
2	4015	100.0	4015	20	AAZ20279	Human telomerase r
3	4015	100.0	4015	20	AAZ00724	Human telomerase c
4	4015	100.0	4015	22	AAH45901	Human hTERT gene.
5	4015	100.0	4015	24	AAH46821	Human telomerase r
6	4015	100.0	4015	24	ABA97534	Cancer cell discr
7	4015	100.0	4015	25	ABZ22474	Human telomerase r
8	4015	100.0	4042	20	AAV72117	Human catalytic te

9	4015	100.0	4070	24	ABU53711
10	4013.4	100.0	4015	20	ABU208150
11	4013.4	100.0	4015	25	AB218391
12	4011.8	99.9	4023	19	ABV60320
13	4007	99.8	4037	19	AAV22428
14	4002	99.7	4027	20	AAK89424
15	4002	99.7	4027	20	AAA29388
16	3956.8	98.6	3964	21	AAK18254
17	3885	96.8	3955	19	AAV22379
18	3872	96.4	3918	20	AAK18269
19	3872	96.4	3918	20	AAK18278
20	3782.8	94.2	3798	19	AAV27876
21	3641	90.7	3855	19	AAV22382
22	3400	84.7	3453	25	ABW76217
23	3400	84.7	3766	24	ADA6790
24	3399	84.7	3399	24	ABZ35720
25	3399	84.7	3399	24	ABX09633
26	3399	84.7	3399	24	ABW78144
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28	3396	84.6	3396	22	AAH44366
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32	3388	84.4	8742	20	ADA67933
33	3278.8	81.7	3500	24	AAK18375
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35	3121	77.7	3167	20	AAK18271
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37	3077.4	76.6	7688	20	AAK18351
38	3073	76.5	3323	20	AAK18277
39	2989.2	72.0	7797	20	AAK18350
40	2843	70.8	3069	20	AAK18276
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42	2837	70.7	2848	19	AAV27872
43	2762.6	68.8	3033	20	AAK18270
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ALIGNMENTS

RESULT 1
AAZ30154
ID AAZ30154 standard; cDNA: 4015 BP.

XX
AC
AAZ30154:XX
DT
26-JAN-2000 (first entry)

XX DE cdNA encoding a human telomerase reverse transcriptase (TRT).

Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
dendritic cell; telomerase activity; cancer cell; proliferating cell;
immunological destruction; telomerase; cancer; proliferation disease;

XX Homo sapiens.

XX	Key	Location/Qualifiers
FH		
FT	CDS	56..3454

XX PN WO9950392-A1.

XX
PD 07-OCT-1999

XX
PF 30-MAR-1999: 99WO-US06898.

XX
PR 31-MAR-1998; 98US-0112006.

XX
PA (GERO-) GERON CORP.

XX Gaeta FCA;
PI
XX
XX
DR WPI; 1999-610845/52.
DR P-FSDB; AAY43621.
XX
XX
PT Eliciting an in vivo immune response for prevention and treatment of
PT cancers -
XX
XX
PS Disclosure; Fig 2; 26pp; English.
XX
XX
CC The present sequence encodes a human telomerase reverse transcriptase
CC (TTR) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TTR peptide in the context of a MHC class I or MHC class
CC II molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TTR gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TTR or to TTR-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used
CC for eliciting an in vivo immune response to telomerase by activating
CC a T lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions.
XX
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match 100.0%; Score 4015; DB 20; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1741	TGTCAGGAGACCACTTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1801	CAAGTTGCAAGCATTTGGAAATCAGACAGACACTTGAAGAGGGTGCACTCGGGAGCTGTC	1860
Db	1801	CAAGTTGCAAGCATTTGGAAATCAGACAGACACTTGAAGAGGGTGCACTCGGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTCAGGACAGCATCGGGAAGCCAGGCCCGCCCTGCTCACGTGCCAGACTCCG	1920
Db	1861	GGAAGCAGAGGTCAGGACAGCATCGGGAAGCCAGGCCCGCCCTGCTCACGTGCCAGACTCCG	1920
QY	1921	CTTCAATCCCAAGCCTGACGGGCTGCGGCCGATGTGAACATGGACTACGTCTGGGAGC	1980
Db	1921	CTTCAATCCCAAGCCTGACGGGCTGCGGCCGATGTGAACATGGACTACGTCTGGGAGC	1980
QY	1981	CAGAAGCTTCCGACAGAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTGTT	2040
Db	1981	CAGAAGCTTCCGACAGAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTGTT	2040
QY	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCCCGCCCTCCTTGGCGCCTCTCTGTCTGG	2100
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCCCGCCCTCCTTGGCGCCTCTCTGTCTGG	2100
QY	2101	CCTGGACGATATCCACAGGGCCTTGGCGCACCTTCTGCTGCTGCTGCTGCTGCTGCG	2160
Db	2101	CCTGGACGATATCCACAGGGCCTTGGCGCACCTTCTGCTGCTGCTGCTGCTGCG	2160
QY	2161	GCGGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGGCGGTACGACACCATTCGCCCA	2220
Db	2161	GCGGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGGCGGTACGACACCATTCGCCCA	2220
QY	2221	GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAACCCCAAGAACACAGTACTGCTGG	2280
Db	2221	GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAACCCCAAGAACACAGTACTGCTGG	2280
QY	2281	TGGGTATGCGGTGTCAGAGGCCGCCATGCGGACGTCGCCGAAGGCCCTTCAAGAGCCA	2340
Db	2281	TGGGTATGCGGTGTCAGAGGCCGCCATGCGGACGTCGCCGAAGGCCCTTCAAGAGCCA	2340
QY	2341	CGTCTCTACTTTCAGACACTCCAGCGGTACATGCGCACAGTTCGTGGCTCAGGACGGA	2400
Db	2341	CGTCTCTACTTTCAGACACTCCAGCGGTACATGCGCACAGTTCGTGGCTCAGGACGGA	2400
QY	2401	GACCACCGCTGAGGGATGCCGTCTCATCGACAGAGCTCCTCCTGAAATGAGGCCAG	2460
Db	2401	GACCACCGCTGAGGGATGCCGTCTCATCGACAGAGCTCCTCCTGAAATGAGGCCAG	2460
QY	2461	CAGTGGCCTCTTGGAGCTTTCTACGCTTCATGTGCCACCGCTGCGCATCAGGGG	2520
Db	2461	CAGTGGCCTCTTGGAGCTTTCTACGCTTCATGTGCCACCGCTGCGCATCAGGGG	2520
QY	2521	CAAGTCTAGCTTCCAGGGATCCCGAGGGCTCCATCTCTCACCGTGTCTG	2580
Db	2521	CAAGTCTAGCTTCCAGGGATCCCGAGGGCTCCATCTCTCACCGTGTCTG	2580
QY	2581	CAGCCTGTGTACGGGACATGGAGAACAGCTGTTTGGGGGATTCGGGGGACGGGCT	2640
Db	2581	CAGCCTGTGTACGGGACATGGAGAACAGCTGTTTGGGGGATTCGGGGGACGGGCT	2640
QY	2641	GCTCTGCGTTTGGTGGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAC	2700
Db	2641	GCTCTGCGTTTGGTGGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAC	2700
QY	2701	CTTCTCAGGACCTGGTCGAGGTGTCCTTGTAGTATGGCTGGTGGTGAACCTTGGCGAA	2760
Db	2701	CTTCTCAGGACCTGGTCGAGGTGTCCTTGTAGTATGGCTGGTGGTGAACCTTGGCGAA	2760
QY	2761	GACAGTGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGGACGCTTTTCTCAGAT	2820
Db	2761	GACAGTGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGGACGCTTTTCTCAGAT	2820
QY	2821	GCCGCCCAACGGCTATTCCCTGTGTGCGGCTGCTGCTGGATACCCGAGCCCTGGAGGT	2880
Db	2821	GCCGCCCAACGGCTATTCCCTGTGTGCGGCTGCTGCTGGATACCCGAGCCCTGGAGGT	2880
QY	2881	GCAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
Db	2881	GCAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGGAGGAACATGCTCGCAAACTTTTGGGGTCTTGGGGTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCTCGCAAACTTTTGGGGTCTTGGGGTGAAGTG	3000
QY	3001	TCACAGCCTGTTTCTGGAATTCAGAGTGAAACAGCCTCCAGAGGCTGTGACCAACATCTA	3060
Db	3001	TCACAGCCTGTTTCTGGAATTCAGAGTGAAACAGCCTCCAGAGGCTGTGACCAACATCTA	3060
QY	3061	CAAGATCTCTCTCTCGAGCGGTACAGGTTTACAGCATGTGCTGCAGCTCCCATTTCA	3120
Db	3061	CAAGATCTCTCTCTCGAGCGGTACAGGTTTACAGCATGTGCTGCAGCTCCCATTTCA	3120
QY	3121	TCAGCAAGTTTGAAGAACCCACATTTTCTTGGCGCTCATCTCTGACACGCTCCCT	3180
Db	3121	TCAGCAAGTTTGAAGAACCCACATTTTCTTGGCGTCTCTCTGACACGCTCCCT	3180
QY	3181	CTGCTACTCTCATCTGAAAGCCCAAGAACGAGGATGTCTGCTGGGGCCCAAGGGCGCGC	3240
Db	3181	CTGCTACTCTCATCTGAAAGCCCAAGAACGAGGATGTCTGCTGGGGCCCAAGGGCGCGC	3240
QY	3241	CGGCTCTGCTCTCGAGCGCTGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3300
Db	3241	CGGCTCTGCTCTCGAGCGCTGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3300
QY	3301	GACTGACACCGTGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3360
Db	3301	GACTGACACCGTGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3360
QY	3361	GCTGAGTCGGAAGCTCCCGGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3420
Db	3361	GCTGAGTCGGAAGCTCCCGGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3420
QY	3421	ACTGCTCTGAGCTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3480
Db	3421	ACTGCTCTGAGCTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3480
QY	3481	GAGCAGACACGACGACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3540
Db	3481	GAGCAGACACGACGACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3540
QY	3541	CACACCCAGCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3600
Db	3541	CACACCCAGCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3600
QY	3601	CATGTCGCTGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3660
Db	3601	CATGTCGCTGAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3660
QY	3661	GAGTGTCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3720
Db	3661	GAGTGTCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3720
QY	3721	GGGCCAGCTTTTCTCACCAGGAGCCGCTTCCACTCCCATAGGAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCTCACCAGGAGCCGCTTCCACTCCCATAGGAATAGTCCATCC	3780
QY	3781	CCAGATTCGCAATGTTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3840
Db	3781	CCAGATTCGCAATGTTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3840
QY	3841	AGGTGAGAGCCTGAGAGGACCTGAGGAGCTCTGGGAAATTTGGAGTACCAAGGTGTG	3900
Db	3841	AGGTGAGAGCCTGAGAGGACCTGAGGAGCTCTGGGAAATTTGGAGTACCAAGGTGTG	3900

QY	3901	CCCTGTACACAGCGGAGGACCCTGCACCTGGATGGGGTCCCCTGTGGGTCAAAATTGGGGG	3961
Db	3901	CCCTGTACACAGCGGAGGACCCTGCACCTGGATGGGGTCCCCTGTGGGTCAAAATTGGGGG	3961
QY	3961	GAGTGCTGTGGGAGTAATAACTGAATATATAGTATATATCAGTTTTCAGTTTGGAAAAA	4015
Db	3961	GAGTGCTGTGGGAGTAATAACTGAATATATAGTATATATCAGTTTTCAGTTTGGAAAAA	4015
 RESULT 2 AAZ20279 ID AAZ20279 standard; cDNA; 4015 BP.			
XX	AC	AAZ20279;	
XX	DT	17-JAN-2000 (first entry)	
XX	DE	Human telomerase reverse transcriptase (hTRT) cDNA.	
XX	KW	Telomerase reverse transcriptase; human; hTRT; cell proliferation;	
XX	KW	cancer; ss.	
XX	OS	Homo sapiens.	
XX	FH	Key Location/Qualifiers	
FT	FT	CDS 56..3454	
FT	FT	/*tag= a	
XX	PN	WO950386-A2.	
XX	PD	07-OCT-1999.	
XX	PF	31-MAR-1999; 99WO-US07097.	
XX	PR	31-MAR-1998; 98US-0052864.	
PR	PR	03-AUG-1998; 98US-0128354.	
XX	PA	(GERO-) GERON CORP.	
XX	PI	Morin GB;	
XX	DR	WPI; 1999-610842/52.	
DR	DR	P-PSDB; AAY32090.	
XX	PT	New catalytic polypeptide and polynucleotide, useful for increasing	
PT	PT	catalytic activity in a cell -	
XX	PS	Disclosure; Fig 2; 24pp; English.	
CC	CC	This is the nucleotide sequence of cDNA encoding human telomerase	
CC	CC	reverse transcriptase (hTRT, see AAY32090). Human telomerase is a	
CC	CC	target for diagnosing and treating diseases relating to cell	
CC	CC	proliferation and senescence, such as cancer, or for increasing	
CC	CC	the proliferative capacity of a cell. A claimed method for	
CC	CC	increasing the proliferative capacity of a vertebrate cell,	
CC	CC	especially a human or other mammalian cell, involves introducing	
CC	CC	into the cell a recombinant hTRT polynucleotide encoding an hTRT	
CC	CC	variant in which residues 192-323, 200-323, 192-271, 200-271,	
CC	CC	222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are	
CC	CC	deleted. A claimed method for reducing telomerase activity in a	
CC	CC	cell involves introducing a recombinant polynucleotide encoding	
CC	CC	an hTRT variant having a deletion of amino acids 192-450, 560-565,	
CC	CC	637-660, 638-660, 748-764 or 1055-1071. The polynucleotides are	
CC	CC	obtained by mutagenesis of the hTRT coding sequence.	
XX	SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;	
 Query Match 100.0%; Score 4015; DB 20; Length 4015; Best Local Similarity 100.0%; Pred No. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GCACGCTCGGTCCTGCTGCGCACGCTGGGAGGCCCTGGCCCCGCCACCCCGCATGCC	60

[illegible]

QY	1141	GACCATCTTTCTGGGTTCCAGGCTTGATGCCAGGACTCCCCGAGGTTGCCCGCCT	1200
DB	1141	GACCATCTTTCTGGGTTCCAGGCTTGATGCCAGGACTCCCCGAGGTTGCCCGCCT	1200
QY	1201	GCCCCAGCCTACTGSCAAATCGGCCCTGTTTCTGAGCTGCTTGGGAACACCGCGCA	1260
DB	1201	GCCCCAGCCTACTGSCAAATCGGCCCTGTTTCTGAGCTGCTTGGGAACACCGCGCA	1260
QY	1261	GTGCCCTACGGGTGCTCCTCAAGACGACATGCCGCTCGAGCTGCGGTCAACCCAGC	1320
DB	1261	GTGCCCTACGGGTGCTCCTCAAGACGACATGCCGCTCGAGCTGCGGTCAACCCAGC	1320
QY	1321	AGCCGGTGTGTGCCCGGAGAACCCAGGGCTGTGTGGGCCCCCGAGGAGGGA	1380
DB	1321	AGCCGGTGTGTGCCCGGAGAACCCAGGGCTGTGTGGGCCCCCGAGGAGGGA	1380
QY	1381	CACAGACCCCGTGCCTGCTGAGCTGCTCGCCAGACAGACGCCCTTGGCAGGTGA	1440
DB	1381	CACAGACCCCGTGCCTGCTGAGCTGCTCGCCAGACAGACGCCCTTGGCAGGTGA	1440
QY	1441	CGGCTTCGTCGGGCTGCTCGCGGCTGTGCTGCCAGGCTCTGGGGTCCAGGCA	1500
DB	1441	CGGCTTCGTCGGGCTGCTCGCGGCTGTGCTGCCAGGCTCTGGGGTCCAGGCA	1500
QY	1501	CAACGACCCGCTTCTCAGGAACACCAAGATTTATCTCCCTGGGGAAGCATGCCAA	1560
DB	1501	CAACGACCCGCTTCTCAGGAACACCAAGATTTATCTCCCTGGGGAAGCATGCCAA	1560
QY	1561	GCTCTCGCTGACGAGCTCACGTGGAAGATGAGCTGCGGGAGTGGCTTGGTGGCAG	1620
DB	1561	GCTCTCGCTGACGAGCTCACGTGGAAGATGAGCTGCGGGAGTGGCTTGGTGGCAG	1620
QY	1621	GAGCCAGGGTGGCTGTGTTCCGCGCAGACACCGCTCTGCTGAGGATCTCTGGC	1680
DB	1621	GAGCCAGGGTGGCTGTGTTCCGCGCAGACACCGCTCTGCTGAGGATCTCTGGC	1680
QY	1681	CAAGTTCTGCACTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1740
DB	1681	CAAGTTCTGCACTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1740
QY	1741	TGTCAGGAGACACGCTTTCAAAAGAACAGGCTCTTTTTCACCGGAAGTGTCTGGAG	1800
DB	1741	TGTCAGGAGACACGCTTTCAAAAGAACAGGCTCTTTTTCACCGGAAGTGTCTGGAG	1800
QY	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCAGCTCGGGAGCTGTC	1860
DB	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCAGCTCGGGAGCTGTC	1860
QY	1861	GGAAGCAGAGTTCAGGCAGCATCGGGAAGCCAGGCCGCTGCTGACGTCCAGACTCG	1920
DB	1861	GGAAGCAGAGTTCAGGCAGCATCGGGAAGCCAGGCCGCTGCTGACGTCCAGACTCG	1920
QY	1921	CTTTCATCCCAAGCCTGACGGCTGGGGCCGATTTGAAATGGACTAGCTGCTGGGAGC	1980
DB	1921	CTTTCATCCCAAGCCTGACGGCTGGGGCCGATTTGAAATGGACTAGCTGCTGGGAGC	1980
QY	1981	CAGAACGTTTCCGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
DB	1981	CAGAACGTTTCCGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTGTCACTAGCAGCGGGGGGGGGCCCGCCCTCTGCTGGGCGCTCTGTGTGGG	2100
DB	2041	CAGCGTGTCACTAGCAGCGGGGGGGGGCCCGCCCTCTGCTGGGCGCTCTGTGTGGG	2100
QY	2101	CGTGGACGATATCCACAGGCGCTGGCGCACCTTCGTGCTGCTGCGGGCCAGGACCC	2160
DB	2101	CGTGGACGATATCCACAGGCGCTGGCGCACCTTCGTGCTGCTGCGGGCCAGGACCC	2160
QY	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGGTGACACACCATCCCGCA	2220
DB	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGGTGACACACCATCCCGCA	2220
QY	2221	GGACAGGCTCAGGAGGTCAATGCCAGCATATCAAAACCCAGAACACAGTACTGCTGCG	2280
DB	2221	GGACAGGCTCAGGAGGTCAATGCCAGCATATCAAAACCCAGAACACAGTACTGCTGCG	2280
QY	2281	TGGGTATCGGTGCTCAGAGAGCCGCCCATGGGACGTCCTGCAAGGCTTCAAGAGCA	2340
DB	2281	TGGGTATCGGTGCTCAGAGAGCCGCCCATGGGACGTCCTGCAAGGCTTCAAGAGCA	2340
QY	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGAGGA	2400
DB	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGAGGA	2400
QY	2401	GACACCCCGCTGAGGATGCTCTCATFCGAGCAGAGCTCTCTCCCTGAATGAGGCCAG	2460
DB	2401	GACACCCCGCTGAGGATGCTCTCATFCGAGCAGAGCTCTCTCCCTGAATGAGGCCAG	2460
QY	2461	CAGTGCCCTTCGACGCTCTCTCATGCTGCTTCCATGCTGCTGCTGCTGCTGCTGCTG	2520
DB	2461	CAGTGCCCTTCGACGCTCTCTCATGCTGCTTCCATGCTGCTGCTGCTGCTGCTGCTG	2520
QY	2521	CAAGTCTTACCTGACGCTGCGAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
DB	2521	CAAGTCTTACCTGACGCTGCGAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
QY	2581	CAGCCTGTGCTACGGGACATGAGAGAACAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
DB	2581	CAGCCTGTGCTACGGGACATGAGAGAACAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
QY	2641	GTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2700
DB	2641	GTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2700
QY	2701	CTTCTCTCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2760
DB	2701	CTTCTCTCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2760
QY	2761	GACAGTGTGAACTTCCCTGTAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2820
DB	2761	GACAGTGTGAACTTCCCTGTAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2820
QY	2821	GCGGGCCACGGCTTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
DB	2821	GCGGGCCACGGCTTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
QY	2881	GCAGCGGCTACTTCCAGCTATGCCCGGACCTCCATCAGAGCAGCTCTCACCTTCAAC	2940
DB	2881	GCAGCGGCTACTTCCAGCTATGCCCGGACCTCCATCAGAGCAGCTCTCACCTTCAAC	2940
QY	2941	CGGCTTCAAGGCTGGGAGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3000
DB	2941	CGGCTTCAAGGCTGGGAGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3000
QY	3001	TCACAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3060
DB	3001	TCACAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3060
QY	3061	CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3120
DB	3061	CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3120
QY	3121	TCAGCAAGTTTGAAGAACCCCATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3180
DB	3121	TCAGCAAGTTTGAAGAACCCCATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3180
QY	3181	CTGCTACTCTTCAATCTGAAAGCCAAAGACGAGGATGCTGCTGCTGCTGCTGCTGCTG	3240
DB	3181	CTGCTACTCTTCAATCTGAAAGCCAAAGACGAGGATGCTGCTGCTGCTGCTGCTGCTG	3240
QY	3241	CGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3300
DB	3241	CGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3300
QY	3301	GACTCGACACCGTGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3360

|||||
3301 GACTCGACACCGTGTACCTAGCTAGTGCACCTCTGGGTCACTCAGGACGCCAGACGCA 3360
QY
3361 GCTGAGTCGGAAGTCTCCGGGGAGCAGCTGACTGCTGCTGAGCCCGAGCCAAACCGCGC 3420
Db
3361 GCTGAGTCGGAAGTCTCCGGGGAGCAGCTGACTGCTGCTGAGCCCGAGCCAAACCGCGC 3420
QY
3421 ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGCCACCCGCCACACAGCCAGGCCGA 3480
Db
3421 ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGCCACCCGCCACACAGCCAGGCCGA 3480
QY
3481 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTACGTCCCGAGGAGGAGGGCGGCC 3540
Db
3481 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTACGTCCCGAGGAGGAGGGCGGCC 3540
QY
3541 CACACCAGGCCCGCAGCTGGAGTCTGAGGCTGAGTGTGTTGGCCCGAGGCGTG 3600
Db
3541 CACACCAGGCCCGCAGCTGGAGTCTGAGGCTGAGTGTGTTGGCCCGAGGCGTG 3600
QY
3601 CATGTCGGGTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAGGGCT 3660
Db
3601 CATGTCGGGTGAAGGCTGAGTGTCCGGCTGAGGAGTGTCCAGCCAGGGCT 3660
QY
3661 GAGTGTCCAGCACACCTCGCGCTTCTACTTCCCGACAGGCTGGCGCTCGGCTCCACCCCA 3720
Db
3661 GAGTGTCCAGCACACCTCGCGCTTCTACTTCCCGACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY
3721 GGGCCAGCTTTCTCACCAGGAGCGCGGCTTCCACTCCCGACATAGGAATAGTCCATCC 3780
Db
3721 GGGCCAGCTTTCTCACCAGGAGCGCGGCTTCCACTCCCGACATAGGAATAGTCCATCC 3780
QY
3781 CCAGATTGCGCATTTGTTACCCCTCGCCCTGCTTCTTCCCGACAGGCTGGCGCTCGGCTCCACCCCA 3840
Db
3781 CCAGATTGCGCATTTGTTACCCCTCGCCCTGCTTCTTCCCGACAGGCTGGCGCTCGGCTCCACCCCA 3840
QY
3841 AGTGGAGACCCCTGAGAGGACCCCTGGAGCTCTGGGAATTTGAGTGTGACCAAGAGTGTG 3900
Db
3841 AGTGGAGACCCCTGAGAGGACCCCTGGAGCTCTGGGAATTTGAGTGTGACCAAGAGTGTG 3900
QY
3901 CCCTGTACAGAGGAGCCCTGCACCTGGATGGGGGTCCTGTGGGTCAAAATTTGGGG 3960
Db
3901 CCCTGTACAGAGGAGCCCTGCACCTGGATGGGGGTCCTGTGGGTCAAAATTTGGGG 3960
QY
3961 GAGTGTCTGTGGAGTAAATATCTGAATATATGATTTTTCAGTTTGTGAAAAAA 4015
Db
3961 GAGTGTCTGTGGAGTAAATATCTGAATATATGATTTTTCAGTTTGTGAAAAAA 4015

RESULT 3
AAZ00724
ID AAZ00724 standard; DNA; 4015 BP.
XX
AC AAZ00724;
XX
DT 06-OCT-1999 (first entry)
XX
DE Human telomerase catalytic domain DNA.
XX
KW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
KW breast cancer; ss.
XX
OS Homo sapiens.
XX
PN DE19804372-A1.
XX
PD 05-AUG-1999.
XX
PF 04-FEB-1998; 98DE-1004372.
XX
PR 04-FEB-1998; 98DE-1004372.
XX

(DAHM/) DAHM M W.
Dahm MW;
WPI; 1999-431408/37.
Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit of telomerase
Example; Fig 1A-B; 26pp; German.
This invention describes a novel method for the quantitation of tumour cells in a body fluid which comprises (1) enrichment or isolation of tumour cells in the sample, (2) amplification of mRNA from these cells that encodes the catalytic subunit of telomerase and (3) quantifying the amount of amplified mRNA. The method is applied to tumour cells derived from (micro)metastases, e.g. associated with a wide range of tumours such as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia, melanoma, pulmonary carcinoma, cancer of colon or breast etc. This sequence encodes a human telomerase protein catalytic domain.
Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
Query Match 100.0%; Score 4015; DB 20; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCGCTGGCTCTCTGCTGGCGACGTGGAGAGCCCTGGCCCGCCACCCCGCGATGCC 60
Db 1 GCAGCGCTGGCTCTCTGCTGGCGACGTGGAGAGCCCTGGCCCGCCACCCCGCGATGCC 60
QY 61 GCGGCTCCCGCTGCGCAGCCGTCCTCTGCTGCGCAGCCTACCCGCGAGTGTCT 120
Db 61 GCGGCTCCCGCTGCGCAGCCGTCCTCTGCTGCGCAGCCTACCCGCGAGTGTCT 120
QY 121 GCCCTGGCCACGTTCTGCGGCGCTGGGCGCCCTGGGCGCCCTGGGCTGGTGCAGCGGG 180
Db 121 GCCCTGGCCACGTTCTGCGGCGCTGGGCGCCCTGGGCGCCCTGGGCTGGTGCAGCGGG 180
QY 181 GGACCCGGCGCTTTCCGCGCGCTGGTGGCCAGTGTGTCGTGCTGGCCTGGGAGCG 240
Db 181 GGACCCGGCGCTTTCCGCGCGCTGGTGGCCAGTGTGTCGTGCTGGCCTGGGAGCG 240
QY 241 ACGGCCCGCCCGCCCGCCCTCTTCCGCGAGTGTCTTCCGCGAGTGTCTTGGAGAGTGTGGC 300
Db 241 ACGGCCCGCCCGCCCGCCCTCTTCCGCGAGTGTCTTCCGCGAGTGTCTTGGAGAGTGTGGC 300
QY 301 CCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAGGAGTGTGCTGGCTTCGGCTTCGC 360
Db 301 CCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAGGAGTGTGCTGGCTTCGC 360
QY 361 GCTGTGGACGGGGCCCGCGGGGCCCTTACACACAGCGCTTCAGCAGCTA 420
Db 361 GCTGTGGACGGGGCCCGCGGGGCCCTTACACACAGCGCTTCAGCAGCTA 420
QY 421 CTGTGCCCAACAGGCTGACCGACCTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGCG 480
Db 421 CTGTGCCCAACAGGCTGACCGACCTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGCG 480
QY 481 CCGGCTGGCGAGCAGCTGCTGCTTACCTGCTGGCAGCTGGCGGCTCTTGTGCTGGT 540
Db 481 CCGGCTGGCGAGCAGCTGCTGCTTACCTGCTGGCAGCTGGCGGCTCTTGTGCTGGT 540
QY 541 GGCTCCCGAGCTGGCGCTTACCGAGTGTGCGGGGCCCGCTGTACACAGCTGCGCGTGCAC 600
Db 541 GGCTCCCGAGCTGGCGCTTACCGAGTGTGCGGGGCCCGCTGTACACAGCTGCGCGTGCAC 600
QY 601 TCAGGGCCCGCCCGCCACAGCTAGTGGACCCCGGAGGCGTGTGGATGCGAACGGCG 660
Db 601 TCAGGGCCCGCCCGCCACAGCTAGTGGACCCCGGAGGCGTGTGGATGCGAACGGCG 660
QY 661 CTGGACCATAGGCTCAGGAGGAGCGGGGCTCCCGCTGGGCTGCCAGCCCGGGTGCAG 720

QY	2881	GCAGGCGACTACTCCAGCTATGCCGAGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940	QY	3961	GAGTGCTGTGGGAGTAAATACTGAATATATGATGATTTTTCAGTTTGAATAAAA	4015
Db	2881	GCAGGCGACTACTCCAGCTATGCCGAGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940	Db	3961	GAGTGCTGTGGGAGTAAATACTGAATATATGATGATTTTTCAGTTTGAATAAAA	4015
QY	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGGCTTTGGGGCTGAAGTG	3000	QY	4015	GAGTGCTGTGGGAGTAAATACTGAATATATGATGATTTTTCAGTTTGAATAAAA	4015
Db	2941	CGGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGGCTTTGGGGCTGAAGTG	3000				
QY	3001	TCACAGCTGTTCTGGATTGACAGTGAACAGCTCCAGAGCTGTCACCAACATCTA	3060	RESULT 4			
Db	3001	TCACAGCTGTTCTGGATTGACAGTGAACAGCTCCAGAGCTGTCACCAACATCTA	3060	AAH45901			
QY	3061	CAAGATCCTCTGCTGACAGGCGTACAGGTTTTCACGCATGTGTGTCAGCTTCCATTTC	3120	ID	AAH45901	standard; DNA; 4015 BP.	
Db	3061	CAAGATCCTCTGCTGACAGGCGTACAGGTTTTCACGCATGTGTGTCAGCTTCCATTTC	3120	XX	AAH45901;		
QY	3121	TCACGAAGTTGGGAAGAACCCACATTTTCTCGGGCTCATCTGACAGGCGCTCCCT	3180	XX	06-SEP-2001	(first entry)	
Db	3121	TCACGAAGTTGGGAAGAACCCACATTTTCTCGGGCTCATCTGACAGGCGCTCCCT	3180	XX	Human hTERT gene.		
QY	3181	CTGCTACTTCCATCTCTGAAGCAAGAACGACGAGGATGTCGTGGGGCCAGAGGCGCGC	3240	XX	Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;		
Db	3181	CTGCTACTTCCATCTCTGAAGCAAGAACGACGAGGATGTCGTGGGGCCAGAGGCGCGC	3240	KW	detection; beta-region; diagnosis; cancer; ds.		
QY	3241	CGGCGCTCTGCGCTCCGAGGCGGTGACGTGCTGTCACCAAGCATTCCTGCTCAAGCT	3300	XX	Homo sapiens.		
Db	3241	CGGCGCTCTGCGCTCCGAGGCGGTGACGTGCTGTCACCAAGCATTCCTGCTCAAGCT	3300	OS			
QY	3301	GACTCGACACCGTCTCACTACGTGCGCACTCTGGGGTCACTAGGACAGCCAGAGCGCA	3360	FH	Key	Location/Qualifiers	
Db	3301	GACTCGACACCGTCTCACTACGTGCGCACTCTGGGGTCACTAGGACAGCCAGAGCGCA	3360	FT	exon	1..274	
QY	3361	GCTGAGTCGGAAGTCCCGGGAGGACGCTGACTGCCCTGGAGGCGGAGGAGGCGCGC	3420	FT	exon	/*tag= a	
Db	3361	GCTGAGTCGGAAGTCCCGGGAGGACGCTGACTGCCCTGGAGGCGGAGGAGGCGCGC	3420	FT	exon	/number= 1	
QY	3421	ACTGCCCTCAGACTTCAAGACCATCTGAGTGTATGGCCACCCCGCCACAGCCAGCGCGA	3480	FT	exon	275..1628	
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTGAGTGTATGGCCACCCCGCCACAGCCAGCGCGA	3480	FT	exon	/*tag= b	
QY	3481	GAGCAGACACAGACGCTGTACGCGGGCTCTACGTCCCGAGGAGGAGGCGCGC	3540	FT	exon	/number= 2	
Db	3481	GAGCAGACACAGACGCTGTACGCGGGCTCTACGTCCCGAGGAGGAGGCGCGC	3540	FT	exon	1629..1824	
QY	3541	CACACCCAGGCGCCGACGCTGGAGTGTAGGCGCTGAGTGAGTGTGTCGCGGAGGCGTG	3600	FT	exon	/*tag= c	
Db	3541	CACACCCAGGCGCCGACGCTGGAGTGTAGGCGCTGAGTGAGTGTGTCGCGGAGGCGTG	3600	FT	exon	/number= 3	
QY	3601	CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCT	3660	FT	exon	1825..2005	
Db	3601	CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCT	3660	FT	exon	/*tag= d	
QY	3661	GAGTGTCCAGCACACCTCCCTCTTCACTTCCACAGGCTGGGCTCGGCTCCACCCCA	3720	FT	exon	/number= 4	
Db	3661	GAGTGTCCAGCACACCTCCCTCTTCACTTCCACAGGCTGGGCTCGGCTCCACCCCA	3720	FT	exon	2006..2185	
QY	3721	GGGCGAGCTTTTCTCACCAGAGGCGCGGCTTCACTCCCGACATAGGAATAGTCCATCC	3780	FT	exon	/*tag= e	
Db	3721	GGGCGAGCTTTTCTCACCAGAGGCGCGGCTTCACTCCCGACATAGGAATAGTCCATCC	3780	FT	exon	/number= 5	
QY	3781	CCAGATTCGCCATTTTCCACCCCTCGCCCTGCGCTTTCCTTCCACCCCGACCATCC	3840	FT	exon	2186..2341	
Db	3781	CCAGATTCGCCATTTTCCACCCCTCGCCCTGCGCTTTCCTTCCACCCCGACCATCC	3840	FT	exon	/*tag= f	
QY	3841	AGGTGGAGACCTTGAGAGGACCTTGGAGTCTGGGAATTTGGAGTGACCAAGGTTGTG	3900	FT	exon	/number= 6	
Db	3841	AGGTGGAGACCTTGAGAGGACCTTGGAGTCTGGGAATTTGGAGTGACCAAGGTTGTG	3900	FT	exon	complement (2309..2325)	
QY	3901	CCCTGTACACAGGCGAGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAATGGGGG	3960	FT	exon	/*tag= g	
Db	3901	CCCTGTACACAGGCGAGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAATGGGGG	3960	FT	exon	/note= "primer SYC1076 (AAH45902) binding site"	
				FT	exon	complement (2311..2325)	
				FT	exon	/*tag= h	
				FT	exon	/note= "primer SYC1118 (AAH45905) binding site"	
				FT	exon	2342..2437	
				FT	exon	/*tag= i	
				FT	exon	/number= 7	
				FT	exon	complement (2345..2374)	
				FT	exon	/*tag= j	
				FT	exon	/bound_moiety= "hybridisation probe CS3"	
				FT	exon	/note= "AAH45908"	
				FT	exon	complement (2427..2456)	
				FT	exon	/*tag= k	
				FT	exon	/bound_moiety= "hybridisation probe CS12"	
				FT	exon	/note= "AAH45906"	
				FT	exon	2438..2523	
				FT	exon	/*tag= l	
				FT	exon	/number= 8	
				FT	exon	complement (2458..2487)	
				FT	exon	/*tag= m	
				FT	exon	/bound_moiety= "hybridisation probe CS1"	
				FT	exon	/note= "AAH45907"	
				FT	exon	2489..2506	
				FT	exon	/*tag= n	
				FT	exon	/note= "primer SYC1097 (AAH45904) binding site"	
				FT	exon	2524..2637	
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				FT	exon	/number= 9	
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				FT	exon	/note= "primer SYC1078 (AAH45903) binding site"	
				FT	exon	2638..2709	

Db	1371	AGCCGGTGTCGTGCCCGGGAGAAAGCCCAAGGGCTCTGTGGCGCCCCCGAGGAGGAGGA	1380
QY	1381	CACAGACCCCGTCGTCCTGGTGTGCACTGCTCCCGCAGCACAGACGCCCTGGCAGGTGA	1440
Db	1381	CACAGACCCCGTCGTCCTGGTGTGCACTGCTCCCGCAGCACAGACGCCCTGGCAGGTGA	1440
QY	1441	CGGCTTCGTGGGGGCTTGCTTGCCCGGGTGGTGGCCCCCAGGCTCTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCGTGGGGGCTTGCTTGCCCGGGTGGTGGCCCCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1501	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAGCATGCCAA	1560
Db	1501	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAGCATGCCAA	1560
QY	1561	GCTCTCGCTCCAGGAGTGAGCTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGGCGAG	1620
Db	1561	GCTCTCGCTCCAGGAGTGAGCTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGGCGAG	1620
QY	1621	GAGCCGAGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTCGTGAGGAGATCCTGGC	1680
Db	1621	GAGCCGAGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTCGTGAGGAGATCCTGGC	1680
QY	1681	CAAGTTCCTGCACGTGGCTGATGAGTGTAGCTGCTGCAGCTGCTCAGGTCTTCTTTTA	1740
Db	1681	CAAGTTCCTGCACGTGGCTGATGAGTGTAGCTGCTGCAGCTGCTCAGGTCTTCTTTTA	1740
QY	1741	TGTCACGGAGACACGTTTCAAAGAAGACAGGCTCTTTTTCACCGAAGAGTCTCTGGAG	1800
Db	1741	TGTCACGGAGACACGTTTCAAAGAAGACAGGCTCTTTTTCACCGAAGAGTCTCTGGAG	1800
QY	1801	CAGTTTCCAAGCANTTGAATTCAGACAGCACTTGAAGAGGGTCAGCTCGGGAGCTGTC	1860
Db	1801	CAGTTTCCAAGCANTTGAATTCAGACAGCACTTGAAGAGGGTCAGCTCGGGAGCTGTC	1860
QY	1861	GGAAGCAGAGTTCAGGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1920
Db	1861	GGAAGCAGAGTTCAGGCAGCATCGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1921	CTTTCATCCCCAAGCCTGACGGGTGCGGCCGATTGTGAACATGACTAGCTCTGGGAGC	1980
Db	1921	CTTTCATCCCCAAGCCTGACGGGTGCGGCCGATTGTGAACATGACTAGCTCTGGGAGC	1980
QY	1981	CAGACGTTCCGAGAGAAAGAGGCGGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040
Db	1981	CAGACGTTCCGAGAGAAAGAGGCGGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040
QY	2041	CAGCGTCTCAACTACGAGGGCGGCGGCCGCCCTCCCTGGGGCCCTCTGTGCTGGG	2100
Db	2041	CAGCGTCTCAACTACGAGGGCGGCGGCCGCCCTCCCTGGGGCCCTCTGTGCTGGG	2100
QY	2101	CCTGGACGATATCCAGAGGCTTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCGAGACCC	2160
Db	2101	CCTGGACGATATCCAGAGGCTTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCGAGACCC	2160
QY	2161	GCGCCTGAGCTGACTTTGTCAAGTGGATGTGACGGGCGGCTACGACACCATCCCCA	2220
Db	2161	GCGCCTGAGCTGACTTTGTCAAGTGGATGTGACGGGCGGCTACGACACCATCCCCA	2220
QY	2221	GGACAGGCTCAGGGAGTTCATCGCCAGCATATCAAAACCCAGACACCATCCCCA	2280
Db	2221	GGACAGGCTCAGGGAGTTCATCGCCAGCATATCAAAACCCAGACACCATCCCCA	2280
QY	2281	TCGGTATGCGTGGTCCAGAAAGGCCCATGGGCAGCTCCGCAAGGCCCTTCAAGAGCA	2340
Db	2281	TCGGTATGCGTGGTCCAGAAAGGCCCATGGGCAGCTCCGCAAGGCCCTTCAAGAGCA	2340
QY	2341	CGTCTCTACTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTCGAGGA	2400
Db	2341	CGTCTCTACTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTCGAGGA	2400
QY	2401	GACCAAGCCGCTCAGGGATGCGGTGCTATCAGACAGAGCTCCTCCCTGAATGAGCCAG	2460
Db	2401	GACCAAGCCGCTCAGGGATGCGGTGCTATCAGACAGAGCTCCTCCCTGAATGAGCCAG	2460

QY 3541 CACACCCAGGCCCGCCAGCCTGGAGTCTGAGGCTGAGTGTGTCGGCGAGGCCCTG 3600
Db |||||||
QY 3541 CACACCCAGGCCCGCCAGCCTGGAGTCTGAGGCTGAGTGTGTCGGCGAGGCCCTG 3600
Db |||||||
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGGCT 3660
Db |||||||
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGGCT 3660
Db |||||||
QY 3661 GAGTGTCCAGCACACTGCGCTTCACTTCCACAGGCTGGCGTCCGCTCCACCCCA 3720
Db |||||||
QY 3721 GGGCCAGCTTTTCCCTCACAGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
Db |||||||
QY 3781 CCAGATTCGCCATTGTTCAACCCTCGCCCTGCTCTTGTGCTTCCACCCACCATCC 3840
Db |||||||
QY 3781 CCAGATTCGCCATTGTTCAACCCTCGCCCTGCTCTTGTGCTTCCACCCACCATCC 3840
Db |||||||
QY 3841 AGGTGGAGACCTTGAGAGGACCTTGGGAGCTCTGGGAATTTGGAGTGACCAAAAGGTGTG 3900
Db |||||||
QY 3841 AGGTGGAGACCTTGAGAGGACCTTGGGAGCTCTGGGAATTTGGAGTGACCAAAAGGTGTG 3900
Db |||||||
QY 3901 CCTGTACACAGCGAGGACCTGCACCTGGATGGGTCCTGTGGTCAAAATGGGG 3960
Db |||||||
QY 3901 CCTGTACACAGCGAGGACCTGCACCTGGATGGGTCCTGTGGTCAAAATGGGG 3960
Db |||||||
QY 3961 GAGGTGCTGTGGGAGTAAATACTGAATATATAGATTTTTCAGTTTGAAGAAAA 4015
Db |||||||
QY 3961 GAGGTGCTGTGGGAGTAAATACTGAATATATAGATTTTTCAGTTTGAAGAAAA 4015
Db |||||||

RESULT 5
AAD46821
ID AAD46821 standard; cdna; 4015 BP.
XX AAD46821;
AC AAD46821;
XX AAD46821;
DT 27-JAN-2003 (first entry)
XX Human telomerase reverse transcriptase (TERT) cdna.
DE Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KW transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KW telomerase reverse transcriptase; gene; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
FT /product= "Human telomerase reverse transcriptase"
XX
PN WO200274948-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-CA003378.
XX
PR 21-MAR-2001; 2001US-277811P.
XX
PA (GERO-) GERON CORP.
XX
PI Denning C, Clark AJ, Schiff JW;
XX
DR WPI; 2002-759895/82.
DR P-PSDB; AAE29226.
XX
PT Mammalian cells, useful for producing animal tissues with carbohydrate
PT antigens that are compatible for transplantation into human patients -
XX
PS Disclosure; Page 33-34; 71pp; English.

XX The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homoyously for expresion of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for producing animal tissue
CC human patients. The present sequence is human telomerase reverse
XX transcriptase (TERT) cdna used in the invention.
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match 100.0%; Score 4015; DB 24; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 60
Db |||||||
QY 1 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 60
Db |||||||
QY 61 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 120
Db |||||||
QY 61 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 120
Db |||||||
QY 121 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 180
Db |||||||
QY 121 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 180
Db |||||||
QY 181 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 240
Db |||||||
QY 181 GCAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 240
Db |||||||
QY 241 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 300
Db |||||||
QY 301 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 360
Db |||||||
QY 301 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 360
Db |||||||
QY 361 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 420
Db |||||||
QY 361 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 420
Db |||||||
QY 421 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 480
Db |||||||
QY 421 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 480
Db |||||||
QY 481 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 540
Db |||||||
QY 481 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 540
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QY 541 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 600
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QY 541 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 600
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QY 601 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 660
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QY 601 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 660
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QY 661 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 720
Db |||||||
QY 661 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 720
Db |||||||
QY 721 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 780
Db |||||||
QY 721 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 780
Db |||||||
QY 781 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 840
Db |||||||
QY 781 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 840
Db |||||||
QY 841 ACAGCGCTCCGCTCCTGCTGCAGCGTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 900
Db |||||||

Db	841	 GCCTGGACCGAGTGAACGTTGTTCTCTGTGTGGTGTCACTTGCACAGACCCGCCGAAGAAGC	900
Qy	901	CACCTCTTTTGGAGGGTGCCTCTCTGSCACGCGCCACTCCACCCATCCGTGTGGCGCGCCA	960
Db	901	CACCTCTTTTGGAGGGTGGCTCTCTGGCAGCGGCCACTCCACCCATCCGTGTGGCGCGCCA	960
Qy	961	GCACACGCGGGGCCCCCAATCCACATCGCGGGCCACACAGCTCCTCTGGACACGCTTGTCTC	1020
Db	961	GCACACGCGGGGCCCCCAATCCACATCGCGGGCCACACAGCTCCTCTGGACACGCTTGTCTC	1020
Qy	1021	CCGGGTACGCGAGACCAAGCACATCTCTACTCTCTACAGGCGACAAGAGAGCAGCTGCG	1080
Db	1021	CCGGGTACGCGAGACCAAGCACATCTCTACTCTCTACAGGCGACAAGAGAGCAGCTGCG	1080
Qy	1081	GCCTCTCCTTCTACTCAGCTTCTTGAGGGCCACGCTTACTTGGGCTCGGAGGCTCTGTGA	1140
Db	1081	GCCTCTCCTTCTACTCAGCTTCTTGAGGGCCACGCTTACTTGGGCTCGGAGGCTCTGTGA	1140
Qy	1141	GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCTCCCGCAGGTTGGCCCGCCT	1200
Db	1141	GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCTCCCGCAGGTTGGCCCGCCT	1200
Qy	1201	GCCCCAGCGCTACTTGGCAATGGGGCCCTGTCTTCTTGGAGCTGCTTGGAGCTGCTGGAG	1260
Db	1201	GCCCCAGCGCTACTTGGCAATGGGGCCCTGTCTTCTTGGAGCTGCTTGGAGCTGCTGGAG	1260
Qy	1261	GTGGCCCTACGGGTGCTCTCAAGAGCACTGCCCGCTCGCAGCTTCGGGTACCCGAGC	1320
Db	1261	GTGGCCCTACGGGTGCTCTCAAGAGCACTGCCCGCTCGCAGCTTCGGGTACCCGAGC	1320
Qy	1321	AGCGGTGCTGTGTGCCGGAGAACCCAGGCTCTGTGGCGGCCCCCGAGAGGAGGA	1380
Db	1321	AGCGGTGCTGTGTGCCGGAGAACCCAGGCTCTGTGGCGGCCCCCGAGAGGAGGA	1380
Qy	1381	CACAGACCCCGCTGCTGTGAGCTGTCTCGCAGCACAGCAGCCCTTGGCAGGTGA	1440
Db	1381	CACAGACCCCGCTGCTGTGAGCTGTCTCGCAGCACAGCAGCCCTTGGCAGGTGA	1440
Qy	1441	CGGCTTCGTGGGCGCTGCTGCGCGGCTGTGCCCCAGGCTCTTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCGTGGGCGCTGCTGCGCGGCTGTGCCCCAGGCTCTTGGGGCTCCAGGCA	1500
Qy	1501	CAACGAACCGGTTCTCTAGGAACACCAAGAAGTTATCTCCTCTGGGAAGCATGCCAA	1560
Db	1501	CAACGAACCGGTTCTCTAGGAACACCAAGAAGTTATCTCCTCTGGGAAGCATGCCAA	1560
Qy	1561	GCCTCTCGCTCAGAGCTGACGTGGAGATGAGCGTGCAGGACTGGCTTGGCTGGCGAG	1620
Db	1561	GCCTCTCGCTCAGAGCTGACGTGGAGATGAGCGTGCAGGACTGGCTTGGCTGGCGAG	1620
Qy	1621	GAGCCAGGGGTTGGCTGTCTTCCGGCCGACAGACCCGTCTCGTGTGGAGATCCTGGC	1680
Db	1621	GAGCCAGGGGTTGGCTGTCTTCCGGCCGACAGACCCGTCTCGTGTGGAGATCCTGGC	1680
Qy	1681	CAAGTTCTCGACTGGCTGATGTGTACGTCTGTCAGCTGGTACAGTCTTCTTTT	1740
Db	1681	CAAGTTCTCGACTGGCTGATGTGTACGTCTGTCAGCTGGTACAGTCTTCTTTT	1740
Qy	1741	TGTACGGACACCGTTTCAAGAAGACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
Db	1741	TGTACGGACACCGTTTCAAGAAGACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
Qy	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGGGAGTGTCT	1860
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGGGAGTGTCT	1860
Qy	1861	GGAAGCAGAGGTTCAGGCAGCATCGGGAAGCCAGSCCGCCCTGCTGACGTCCAGACTCCG	1920
Db	1861	GGAAGCAGAGGTTCAGGCAGCATCGGGAAGCCAGSCCGCCCTGCTGACGTCCAGACTCCG	1920
Qy	1921	CTTTCATCCCAAGCCTGACGGCTGCGGCCGATTTGTGAACATGAATACGTCTGGAGC	1980

Qy	3061	CAAGATCCTCTGCTGACAGCGGTACAGGTTTCACGANTGTGCTGACAGTCCCAATTCA	3120
Db	3061	CAAGATCCTCTGCTGACAGCGGTACAGGTTTCACGANTGTGCTGACAGTCCCAATTCA	3120
Qy	3121	TCAGCAAGTTTGGAAAGACCCACATTTTTCCTGCGGTCATCTCTGACAGGCGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGGTCATCTCTGACAGGCGCTCCCT	3180
Qy	3181	CTGCTACTCCTCTGAAAGCCAAAGACGACGAGGATGTCGCTGGGGCCAAAGGCGCGCG	3240
Db	3181	CTGCTACTCCTCTGAAAGCCAAAGACGACGAGGATGTCGCTGGGGCCAAAGGCGCGCG	3240
Qy	3241	CGGCGCTCTGCGCTCCGAGCGGTGACGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
Db	3241	CGGCGCTCTGCGCTCCGAGCGGTGACGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
Qy	3301	GACTCGACACCGTGTCACTTACCTTGCACATCTCTGGGTCTACTCAGACAGCCAGACGCA	3360
Db	3301	GACTCGACACCGTGTCACTTACCTTGCACATCTCTGGGTCTACTCAGACAGCCAGACGCA	3360
Qy	3361	GCTGAGTCGGAAGTCCCGGGGACGAGCTGACTGCGCTTGAGGCGCGACGCCAACCCGGC	3420
Db	3361	GCTGAGTCGGAAGTCCCGGGGACGAGCTGACTGCGCTTGAGGCGCGACGCCAACCCGGC	3420
Qy	3421	ACTGCCCTCAGACTTCAAGACATCTCTGGACTGATGGCCACC GCCCACAGCGCCGGA	3480
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACC GCCCACAGCGCCGGA	3480
Qy	3481	GAGCAGACACACAGACCCCTGCACGCCGGGCTTACGTCCTCCAGGAGGGGGGGCGGC	3540
Db	3481	GAGCAGACACACAGACCCCTGCACGCCGGGCTTACGTCCTCCAGGAGGGGGGGCGGC	3540
Qy	3541	CACACCCAGGCCGACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCGCTG	3600
Db	3541	CACACCCAGGCCGACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCGCTG	3600
Qy	3601	CATGTCGGGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
Db	3601	CATGTCGGGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
Qy	3661	GAGTGTCCAGCACACCTTCCGCTTCTACTTCCCCACAGGCTGCGCTCGGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGCACACCTTCCGCTTCTACTTCCCCACAGGCTGCGCTCGGCTCCACCCCA	3720
Qy	3721	GGGCCAGCTTTTCTCACCAGGACCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCTCACCAGGACCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
Qy	3781	CCAGATTCCGCATTTGTTACCCCTCGCCCTGCGCTTTCGCTTCCACCCCAACATCC	3840
Db	3781	CCAGATTCCGCATTTGTTACCCCTCGCCCTGCGCTTTCGCTTCCACCCCAACATCC	3840
Qy	3841	AGGTGGAGACCTTGAGAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG	3900
Db	3841	AGGTGGAGACCTTGAGAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG	3900
Qy	3901	CCCTGTATACAGCGGAGGACCCCTGCACCTTGGATGGGGTCCCTGTGGTCAAAATTTGGGG	3960
Db	3901	CCCTGTATACAGCGGAGGACCCCTGCACCTTGGATGGGGTCCCTGTGGTCAAAATTTGGGG	3960
Qy	3961	GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTTCAGTTTTTGAAAAAA	4015
Db	3961	GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTTCAGTTTTTGAAAAAA	4015

RESULT 6
ABA97534
ID ABA97534 standard; DNA; 4015 BP.
XX
XX ABA97534;
XX
DT 05-APR-2002 (first entry)

XX	Cancer cell discrimination method related human DNA.
DE	
XX	
KW	Human; telomerase; enzyme; cancer cell discrimination; gene;
KW	reverse transcriptase; ds.
XX	
OS	Homo sapiens.
XX	
PN	JP2001309791-A.
XX	
PD	06-NOV-2001.
XX	
PF	02-MAY-2000; 2000JP-0138250.
XX	
PR	02-MAY-2000; 2000JP-0138250.
XX	
PA	(KANE/) KANEUCHI H.
PA	(KAMI/) KAMIMORI M.
XX	
DR	WPI; 2002-134853/18.
XX	
PT	Discrimination of a cancer cell in a sample tissue, comprises
PT	determining the expression level of a reverse transcriptase component
PT	of telomerase using a hybridization assay -
XX	
PS	Claim 2; Page 9-10; 16pp; Japanese.
XX	
CC	The present invention relates to a method for the discrimination of a
CC	cancer cell in a sample tissue, which involves determining the expression
CC	level of a reverse transcriptase component of telomerase in a cell
CC	constituting the sample tissue by an in situ hybridization of the mRNA of
CC	the enzyme, and judging a cell showing a higher expression level than
CC	that of the reverse transcriptase component of telomerase in a normal
CC	cell to be a cancer cell. The present sequence is a human DNA used in the
CC	exemplification of the invention.
XX	
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match	100.0%;	Score 4015;	DB 24;	Length 4015;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 4015;	Conservative	0;	Mismatches	0; Indels	0; Gaps
QY	1	GCAGGCTGGCTGCTGCGACACTGGGAAGCCCTGGCCCGGGCCACCCCGCGATGCC	60		
DB	1	GCAGGCTGGCTGCTGCGACACTGGGAAGCCCTGGCCCGGGCCACCCCGCGATGCC	60		
QY	61	GGCGCTCCCGCTGCCGAGCGGTGGCTCCCTGCTGCGACGCACTACCGCGAGGTGCT	120		
DB	61	GGCGCTCCCGCTGCCGAGCGGTGGCTCCCTGCTGCGACGCACTACCGCGAGGTGCT	120		
QY	121	GCCGCTGCCACGTTCTGTCGGCGCTGGGGCCCCAGGCGTGGTGCAGCGCGG	180		
DB	121	GCCGCTGCCACGTTCTGTCGGCGCTGGGGCCCCAGGCGTGGTGCAGCGCGG	180		
QY	181	GGACCCGGGGCTTTCGGGGCGCTGGTGCCCACTGCTGCTGGTGGCTGCCCTGGACGC	240		
DB	181	GGACCCGGGGCTTTCGGGGCGCTGGTGCCCACTGCTGCTGGTGGCTGGGACGC	240		
QY	241	ACGGCGGCCCGCGCGGCCCTCTCTCGCCAGGTGTCCTGGCTGAAGGAGCTGGTGGC	300		
DB	241	ACGGCGGCCCGCGCGGCCCTCTCTCGCCAGGTGTCCTGGCTGAAGGAGCTGGTGGC	300		
QY	301	CCGAGTGTGCAGAGGCTGTGGCAGCGGGCGCGAAGACGTGCTGGCTTCGGCTTCGC	360		
DB	301	CCGAGTGTGCAGAGGCTGTGGCAGCGGGCGCGAAGACGTGCTGGCTTCGGCTTCGC	360		
QY	361	GCTGCTGGACGGGGCCCGGGGGCCCCCGGAGGCTTCACACACAGCGTGGCAGCTA	420		
DB	361	GCTGCTGGACGGGGCCCGGGGGCCCCCGGAGGCTTCACACACAGCGTGGCAGCTA	420		
QY	421	CCTGCCAACACGGTGAACGACACTCTGGGGGAGCGGGGCTGCTGCTGGC	480		
DB	421	CCTGCCAACACGGTGAACGACACTCTGGGGGAGCGGGGCTGCTGCTGGC	480		

QY	481	CCGCGTGGCGACGAGCTGCTGTGTTCACTCTGTGTCACGCTGCGCGCTCTTTTGTGCTGGT	540
DB	481		
QY	481	CCGCGTGGCGACGAGCTGCTGTGTTCACTCTGTGTCACGCTGCGCGCTCTTTTGTGCTGGT	540
QY	541	GGCTCCACGCTGGCTACCAAGTGTGGGGCGCGCTGTACCAGCTTCGGCGCTGCCAC	600
DB	541		
QY	541	GGCTCCACGCTGGCTACCAAGTGTGGGGCGCGCTGTACCAGCTTCGGCGCTGCCAC	600
QY	601	TCAGGCGCGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATCGCAACGGC	660
DB	601		
QY	661	CTGGAACCATAGGCTCAGGAGCGCGGGTCCCTCTGGCTGCCAGCCCGGGTGGAG	720
DB	661		
QY	721	GAGCGCGGGGCACTGCCAGCGCAAGTCTGCGTGTGCCAAGAGGCCACGCGCTGGCGC	780
DB	721		
QY	781	TGCCCCGTGACCGGAGCGGACGCCGCTTGGGACGGGCTCTTGGGCCACCCGGGACGAC	840
DB	781		
QY	841	CGCTGACGAGTACCGCTGCTGTGTGTGTCACTGCGACACCGCGCAAGAAGC	900
DB	841		
QY	901	CACCTCTTTGGAGGCTGCGCTCTTGGCACGCGGCACCTCCCAACCATCCGTGGGCGGCA	960
DB	901		
QY	961	GCACGAGGGGCCCCCATCCACATCGCGGCGCACAGCTCCCTGGGACACGCTTGTCC	1020
DB	961		
QY	1021	CCGCGTGTAGCGGAGACCAAGCACTTCTACTCTTACGCGACAAAGGACGAGCTGCG	1080
DB	1021		
QY	1081	GGCTCTCTTACTACTGCTCTGAGGCGCGAGCTGAGTGGCTCGGAGGCTGTGGA	1140
DB	1081		
QY	1141	GACCATCTTCTGGGTTCCAGGCGCTGATGCCAGGACTCCCGCAGAGTTGCCCGGCT	1200
DB	1141		
QY	1201	GGCCAGCGCTACTGGAAATGGGGCCCTGTTCTGTGAGCTGTCTGGGAACCGCGCA	1260
DB	1201		
QY	1261	GTGCCCCCTACGGGCTCTCTCAAGACGACACTGCCGCTGCGAGCTGGGTCACCCACG	1320
DB	1261		
QY	1321	AGCCGGTGTGTGCCCCGGGAGAAGCCACAGGCTCTGTGGGGCCCCCGGAGGAGGA	1380
DB	1321		
QY	1381	CACAGACCCCGTGGCTGTGAGTGTTCGCGCCAGCACAGCAGCCCTTGCAGGTTA	1440
DB	1381		
QY	1441	CGGCTCTGTGGGCGCTGCTGCGCGGGTGTGTGCCCGAGGCTCTTGGGGTCCAGGCA	1500
DB	1441		
QY	1501	CAACGAAGCGCTTCTCAGGAACACCAAGAAGTTTCATCTCGCTGGGGAGCATGCCAA	1560
DB	1501		
QY	1561	GCTCTCGCTGACGAGCTGACGTGGAAATGACGCTGGGAGTGCCTTTGGCTGCCGAC	1620
DB	1561		
QY	1621	GAGCCACAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTCGGTGAGGAGATCCCTGGC	1680
DB	1621		
QY	1681	CAAGTTCTTGCACTGGCTGTACGTGTGAGTGTGTCAGGTGTCAGGTCTTCTTTT	1740
DB	1681		
QY	1741	TGTACGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
DB	1741		
QY	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCAGCTTGGGAGCTGC	1860
DB	1801		
QY	1861	GGAAAGAGGTCAGGACAGTCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACCTCCG	1920
DB	1861		
QY	1921	CTTATCTCCCAAGCCTGACGGGCTCGGCCGATTGTGAACATGACCTACGCTGGGAGC	1980
DB	1921		
QY	1981	CAGAGCTTCCCGAGAAAAGAGGGCGAGCGTCTACCTCGAGGGTGAAGGACACTGTT	2040
DB	1981		
QY	2041	CAGCGTGTCTAACTACGAGCGGCGCGGCCCGCCCTCTGGCGGCTCTGTGCTGGG	2100
DB	2041		
QY	2101	CCTGGACGATATCCACAGGGCCTGCGCACCTTCTGCTGTGCTGTGGCGCTCTGTGCTGGG	2160
DB	2101		
QY	2161	GCGCGCTGAGCTGTACTTTGTCAGGTGGATGACGGCGCTACGACACCATCCGCCA	2220
DB	2161		
QY	2221	GGACGGCTCAGGAGGTTCATCGCAGCATATCAAAACCCAGAACACGTAAGTGGTGGG	2280
DB	2221		
QY	2281	TCGGTATCGGTGTCAGAAAGCGCCCATGGGACGCTCGCAAGGCTTCAAGAGGCA	2340
DB	2281		
QY	2341	CGTCTCTACTCTCAGACAGCTCCAGCGCTACATGGCAGAGTTCTGGCTCACCTGCAGGA	2400
DB	2341		
QY	2401	GACACCGCGCTGAGGGATGCGGTGTATCAGCAGAGCTCCTCCCTGAATGAGGCGAG	2460
DB	2401		
QY	2461	CAGTGGCTCTTCGAGCTCTTCTACGCTTCATGTGCCACACGCGCTGCGCATCAGGGG	2520
DB	2461		
QY	2521	CAAGTCTTACGTCAGGATCCCGAGGGCTCCAPCTCTCCACGCTGCTCTG	2580
DB	2521		
QY	2581	CAGCTGTGCTACGGGACATGGGAACAAGCTGTTTGGGGGATTCGCGGAGCGGCT	2640
DB	2581		
QY	2641	GCTCCTGCGCTTTGGTGGATGATTCTTGTGTGGTGACCTCACTCACCCACGCGAAGAC	2700
DB	2641		

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Db 2641 GCTCTGCGTTGGTGGATGATTCTGTGGTGACACCTCACCTCACCCACCGGAAC 2700
QY 2701 CTTCTCAGAGCCCTGGTCCGAGGTGCTCCTGAGTATGGCTGGTGAACCTTGGCGAA 2760
Db 2701 CTTCTCAGAGCCCTGGTCCGAGGTGCTCCTGAGTATGGCTGGTGAACCTTGGCGAA 2760
QY 2761 GACAGTGGTGAACCTCCCTGTAGAACAGAGCCCTGGTGGACAGCGCTTTGTTTCAGAT 2820
Db 2761 GACAGTGGTGAACCTCCCTGTAGAACAGAGCCCTGGTGGACAGCGCTTTGTTTCAGAT 2820
QY 2821 GCCGGCCACAGCGCTATTCCCTGTGGTGGCGCTGCTGTGATACCCGACCCCTGAGGT 2880
Db 2821 GCCGGCCACAGCGCTATTCCCTGTGGTGGCGCTGCTGTGATACCCGACCCCTGAGGT 2880
QY 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2941 CGGCTTCAAGGCTGGGAGGAACATGGTGCAGAACTCTTTGGGGTCTTGGGGTGAAGTG 3000
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGGTGCAGAACTCTTTGGGGTCTTGGGGTGAAGTG 3000
QY 3001 TCACAGCGCTTCTGATTTGAGGTGAACAGCCCTCCAGAGCGTGTGCACCAACATCTA 3060
Db 3001 TCACAGCGCTTCTGATTTGAGGTGAACAGCCCTCCAGAGCGTGTGCACCAACATCTA 3060
QY 3061 CAAGATCCCTGCTGACGCGCTACAGTTTACGCAATGTGCTGCAGTCCCATTTCA 3120
Db 3061 CAAGATCCCTGCTGACGCGCTACAGTTTACGCAATGTGCTGCAGTCCCATTTCA 3120
QY 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGCGCTCCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGCGCTCCCT 3180
QY 3181 CTGCTACTCATCTCTGAAAGCAAGACGAGGATGCTGCGGGGCCAAGGGCCCGC 3240
Db 3181 CTGCTACTCATCTCTGAAAGCAAGACGAGGATGCTGCGGGGCCAAGGGCCCGC 3240
QY 3241 CGGCGCTCTGCGCTCGAGGCGCTGAGTGGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
Db 3241 CGGCGCTCTGCGCTCGAGGCGCTGAGTGGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
QY 3301 GACTCGACACCTGTACCTAGTGCCTACTCTGGGGTCACTCAGACAGCCAGACGCA 3360
Db 3301 GACTCGACACCTGTACCTAGTGCCTACTCTGGGGTCACTCAGACAGCCAGACGCA 3360
QY 3361 GCTGAGTGGAGCTCCCGGGACGACGCTGACTGCTGGAGCGCGCAGCCACCCGCG 3420
Db 3361 GCTGAGTGGAGCTCCCGGGACGACGCTGACTGCTGGAGCGCGCAGCCACCCGCG 3420
QY 3421 ACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCCACAGCCAGCCGA 3480
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCCACAGCCAGCCGA 3480
QY 3481 GAGCAGACACAGACCCCTGTACCCCGGCTCTACGTCCTCAGGAGGAGGGGGCGCC 3540
Db 3481 GAGCAGACACAGACCCCTGTACCCCGGCTCTACGTCCTCAGGAGGAGGGGGCGCC 3540
QY 3541 CACACCCAGGCGCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGCGCGAGGCGCTG 3600
Db 3541 CACACCCAGGCGCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGCGCGAGGCGCTG 3600
QY 3601 CATGTCGGCTGAAGCTGAGTGTGCGGTGAGGCTGAGCGAGTGTCCAGCCCAAGGGCT 3660
Db 3601 CATGTCGGCTGAAGCTGAGTGTGCGGTGAGGCTGAGCGAGTGTCCAGCCCAAGGGCT 3660
QY 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCACAGCGCTGGCGTCCGGCTCCACCCCA 3720
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCACAGCGCTGGCGTCCGGCTCCACCCCA 3720
QY 3721 GGGCCAGCTTTTCTCACCAGAGCCCGGCTTCCACTCCCATAGGAATAGTCCATCC 3780
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Db 3721 GGCCAGCTTTTCTCACCAGAGCCCGGCTTCCACTCCCATAGGAATAGTCCATCC 3780
QY 3781 CCAGATTGCAATGTTTCAACCCCTGCGCTGCGCTTCTTTCCTTCCACCCCAACATCC 3840
Db 3781 CCAGATTGCAATGTTTCAACCCCTGCGCTGCGCTTCTTTCCTTCCACCCCAACATCC 3840
QY 3841 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
Db 3841 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
QY 3901 CCCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATGGGG 3960
Db 3901 CCCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATGGGG 3960
QY 3961 GAGTGTCTGTGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAAAA 4015
Db 3961 GAGTGTCTGTGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAAAA 4015

RESULT 7
ABZ22474
ID ABZ22474 standard; cDNA; 4015 BP.
XX
AC ABZ22474;
XX
DT 25-MAR-2003 (first entry)
XX
Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.
XX
Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW vulvular; antitumor; epithelial cell migration promoter; wound;
KW epithelial; skin wound; lesion; burn; surgical incision; ulcer;
KW epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 56..3454
FT /*tag= a
FT /product= "human telomerase reverse transcriptase"
XX
XX WO200291999-A2.
XX
PD 21-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US14867.
XX
PR 09-MAY-2001; 2001US-289903P.
XX
PA (GERO-) GERON CORP.
XX
PI Jiang X, Chiu C, Harley CB;
XX
DR WPI; 2003-120591/11.
XX
P-PSDB; ABP56676.
XX
Composition for treating wounds and enhancing epithelialization of a skin
surface, comprises vector encoding telomerase reverse transcriptase or
telomerase epithelial cells on a microparticle or a matrix -
XX
Disclosure; Page 31-32; 68pp; English.
XX
The present invention describes a pharmaceutical composition (I)
comprising a vector encoding telomerase reverse transcriptase (TERT) in
an excipient or device, or comprises telomerase epithelial cells on a
microparticle or a matrix suitable for topical administration or
administration to a wound site. (I) has vulvular and antitumor
activities and can be used to promote epithelial cell migration. (I) is
useful for treating a wound and enhancing epithelialization of a skin
surface. The wound is especially skin wound including acute lesion such
as traumatic lesion, burn, or surgical incision, chronic lesion such as
chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
is further monitored for closure. The telomerase activity or TERT
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expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding hTERT is useful for the preparation of a medicament for treatment of a wound on an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (1) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence encodes human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5.

Query Match 100.0%; Score 4015; DB 25; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCAGCGTCCCGTCTGTCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 120
1 GCAGCGTCCCGTCTGTCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 120
61 GCGCGTCCCGTCTGTCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 120
61 GCGCGTCCCGTCTGTCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 120
121 GCGCGTCCCGTCTGTCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 180
121 GCGCGTCCCGTCTGTCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 180
181 GGACCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 240
181 GGACCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 240
241 ACGGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 300
241 ACGGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 300
301 CCGAGTCTCGAGAGGTGTCGAGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGT 360
301 CCGAGTCTCGAGAGGTGTCGAGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGT 360
361 GCTGCTGAGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGT 420
361 GCTGCTGAGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGT 420
421 CCGTCCCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 480
421 CCGTCCCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 480
481 CCGCGTGGCGCGAGCTGCTGTCACCTGCTGCGACGCTGCGCTCCCTGCTGCGCAGGTGCT 540
481 CCGCGTGGCGCGAGCTGCTGTCACCTGCTGCGACGCTGCGCTCCCTGCTGCGCAGGTGCT 540
541 GCGTCCCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 600
541 GCGTCCCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 600
601 TCAGGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 660
601 TCAGGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 660
661 CTGGAACCATAGCGTCAGGAGCGCGGTGCTCCCTGCGCGCTGCGCTCCCTGCTGCGCAGGT 720
661 CTGGAACCATAGCGTCAGGAGCGCGGTGCTCCCTGCGCGCTGCGCTCCCTGCTGCGCAGGT 720
721 GAGGCGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 780
721 GAGGCGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 780
781 TGCGCTGAGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGT 840

Db 781 TGCGCTGAGCGCGCGCTTTCGCGCGCTGCGCTCCCTGCGCGCTGCGCTCCCTGCGCAGGTGCT 840
Qy 841 GCGTGGACCGAGTACCGTGGTCTTCTGCTGGTGTACCTGCGCAGACCCCGCGAAGACG 900
Db 841 GCGTGGACCGAGTACCGTGGTCTTCTGCTGGTGTACCTGCGCAGACCCCGCGAAGACG 900
Qy 901 CACCTCTTTTGAGAGGTGCGTCTCTGCGACGCGCCACTCCCAACCATCTCCGTGGCGCGCA 960
Db 901 CACCTCTTTTGAGAGGTGCGTCTCTGCGACGCGCCACTCCCAACCATCTCCGTGGCGCGCA 960
Qy 961 GCACCG 1020
Db 961 GCACCG 1020
Qy 1021 CCGCGGTACCG 1080
Db 1021 CCGCGGTACCG 1080
Qy 1081 GCGCTCTTCTTCTACTCAGCTCTCTGAGGCGCGCGCTGACTGGGCGCTCGGAGGCTCGTGA 1140
Db 1081 GCGCTCTTCTTCTACTCAGCTCTCTGAGGCGCGCGCTGACTGGGCGCTCGGAGGCTCGTGA 1140
Qy 1141 GACCATCTTTCGCGGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Db 1141 GACCATCTTTCGCGGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Qy 1201 GCGCGAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
Db 1201 GCGCGAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
Qy 1261 GTGCGCGTACGCGGTGCTCTCAAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Db 1261 GTGCGCGTACGCGGTGCTCTCAAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Qy 1321 AGCGGTGCTGTCGCCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Db 1321 AGCGGTGCTGTCGCCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Qy 1381 CACAGACCG 1440
Db 1381 CACAGACCG 1440
Qy 1441 CCGCGTTCGTCG 1500
Db 1441 CCGCGTTCGTCG 1500
Qy 1501 CAACGAACCGCGCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCGAA 1560
Db 1501 CAACGAACCGCGCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCGAA 1560
Qy 1561 GCTCTGCTGCGAGGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGGCGAG 1620
Db 1561 GCTCTGCTGCGAGGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGGCGAG 1620
Qy 1621 GAGCGAGGCTTGGCTGCTTCCGCGCGCGAGACCGCTGCTGGTGGAGAGATCTTGGC 1680
Db 1621 GAGCGAGGCTTGGCTGCTTCCGCGCGCGAGACCGCTGCTGGTGGAGAGATCTTGGC 1680
Qy 1681 CAAGTTCCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 CAAGTTCCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Qy 1741 TGTCAGGAGACACCGTTCG 1800
Db 1741 TGTCAGGAGACACCGTTCG 1800
Qy 1801 CAAGTTCGAGAGATGGAATCAGACAGCTTGAAGAGGCTGCGAGTGGGAGGCTGTC 1860
Db 1801 CAAGTTCGAGAGATGGAATCAGACAGCTTGAAGAGGCTGCGAGTGGGAGGCTGTC 1860
Qy 1861 GGAAGCAGAGCTCAGGCGAGCATCGGGAAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Db 1861 GGAAGCAGAGCTCAGGCGAGCATCGGGAAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920

QY	1261	GTCCCTACGGGGTCTCTCAAGACGCACACTGCCCGCTGCGAGCTGCGGTCAACCCAGC	1320
Db	1268	GTCCCTACGGGGTCTCTCAAGACGCACACTGCCCGCTGCGAGCTGCGGTCAACCCAGC	1327
QY	1321	AGCCGGTGTGTGCCCGGAGAACCCAGAGGCTCTGTGGCGGCCCGGAGGAGGA	1380
Db	1328	AGCCGGTGTGTGCCCGGAGAACCCAGAGGCTCTGTGGCGGCCCGGAGGAGGA	1387
QY	1381	CACAGACCCCGCTGCGCTGTGTGAGCTGTCTCCGCCACACAGAGCCCTTGGCAGGTGTA	1440
Db	1388	CACAGACCCCGCTGCGCTGTGTGAGCTGTCTCCGCCACACAGAGCCCTTGGCAGGTGTA	1447
QY	1441	CGGCTTGTGCGGGCTGCTGCGCGGCTGTGTGCGGCCAGGCTCTGGGGCTTCCAGGCA	1500
Db	1448	CGGCTTGTGCGGGCTGCTGCGCGGCTGTGTGCGGCCAGGCTCTGGGGCTTCCAGGCA	1507
QY	1501	CAACGAACGCCCTTCTCAGGAACACCAAGAGATTCATCTCCCTGGGGAAGCATGCCAA	1560
Db	1508	CAACGAACGCCCTTCTCAGGAACACCAAGAGATTCATCTCCCTGGGGAAGCATGCCAA	1567
QY	1561	GCTCTCGCTGCAGAGCTGACGTGGAGATGAGCGTGGGGACTGGGCTTGGCTGGCGAG	1620
Db	1568	GCTCTCGCTGCAGAGCTGACGTGGAGATGAGCGTGGGGACTGGGCTTGGCTGGCGAG	1627
QY	1621	GAGCCAGGGTGGCTGTGTTCCGGCCGACAGACCGTCTGCGTGAGGAGATCTTGGC	1680
Db	1628	GAGCCAGGGTGGCTGTGTTCCGGCCGACAGACCGTCTGCGTGAGGAGATCTTGGC	1687
QY	1681	CAAGTTCCTGCACTGCTGATGATGTGTACGTCGTCGAGCTCTCAGGCTCTTCTTTTA	1740
Db	1688	CAAGTTCCTGCACTGCTGATGATGTGTACGTCGTCGAGCTCTCAGGCTCTTCTTTTA	1747
QY	1741	TGTCACGGAGACACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTTGAG	1800
Db	1748	TGTCACGGAGACACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTTGAG	1807
QY	1801	CAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGTCAGCTGCGGAGTGTG	1860
Db	1808	CAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGTCAGCTGCGGAGTGTG	1867
QY	1861	GGAAGCAGAGTTCAGCAGCATCGGAAGCAGCGCCGCTCTGACGTCACAGATCCG	1920
Db	1868	GGAAGCAGAGTTCAGCAGCATCGGAAGCAGCGCCGCTCTGACGTCACAGATCCG	1927
QY	1921	CTTTCATCCCAAGCCTCAGCGGCTGCGCGGATTTGTAACATGGACTACGCTGCGGAGC	1980
Db	1928	CTTTCATCCCAAGCCTCAGCGGCTGCGCGGATTTGTAACATGGACTACGCTGCGGAGC	1987
QY	1981	CAGAAGTTCGCGAGAGAAAGAGGCGCGAGCGCTCTCACCTCAGGGTGAAGGCACGTGT	2040
Db	1988	CAGAAGTTCGCGAGAGAAAGAGGCGCGAGCGCTCTCACCTCAGGGTGAAGGCACGTGT	2047
QY	2041	CAGCGTGTCAACTACGAGCGGCGCGCGCCGCTCTGCGGCGCCCTCTGTGTGGG	2100
Db	2048	CAGCGTGTCAACTACGAGCGGCGCGCGCCGCTCTGCGGCGCCCTCTGTGTGGG	2107
QY	2101	CTTGGACGATATCCACAGGSCCTGGCGACCTTCTGTCGTCGTCGTCGTCGTCGTCGTC	2160
Db	2108	CTTGGACGATATCCACAGGSCCTGGCGACCTTCTGTCGTCGTCGTCGTCGTCGTCGTC	2167
QY	2161	GCCGCTGAGCTGTACTTTGTAAGTGTGATGTAGCGGGCGGTACGACACATTCGCCCA	2220
Db	2168	GCCGCTGAGCTGTACTTTGTAAGTGTGATGTAGCGGGCGGTACGACACATTCGCCCA	2227
QY	2221	GGAAGGCTCAGGAGTATCCCGACATCATCAAAACCCAGAACACGTAAGTGTGCGG	2280
Db	2228	GGAAGGCTCAGGAGTATCCCGACATCATCAAAACCCAGAACACGTAAGTGTGCGG	2287
QY	2281	TCGGTATGCGGTGTCAGAGGCGCCCGCTTGGGCTGCTGCGGAGGCTTCAAGAGCCA	2340
Db	2288	TCGGTATGCGGTGTCAGAGGCGCCCGCTTGGGCTGCTGCGGAGGCTTCAAGAGCCA	2347
QY	2341	CGTCTCTACCTTGCAGACCTCAGCGGTACATGCGACAGTTCTGTGGCTCACCTGCAGGA	2400
Db	2348	CGTCTCTACCTTGCAGACCTCAGCGGTACATGCGACAGTTCTGTGGCTCACCTGCAGGA	2407
QY	2401	GACCAGCCGCTCAGGATGCCCTCTCATCGAGCAGAGCTCTCCTCTGATGAGGCCAG	2460
Db	2408	GACCAGCCGCTCAGGATGCCCTCTCATCGAGCAGAGCTCTCCTCTGATGAGGCCAG	2467
QY	2461	CAGTGGCCTCTTGCAGGCTCTTCTTACGCTTCACTGTGTCACACGCGTGCCTACAGGGG	2520
Db	2468	CAGTGGCCTCTTGCAGGCTCTTCTTACGCTTCACTGTGTCACACGCGTGCCTACAGGGG	2527
QY	2521	CAAGTCTCAGCTCAGTGCAGGGGATCCCGAGGGTTCATCTCTTCCACGCTGTCTG	2580
Db	2528	CAAGTCTCAGCTCAGTGCAGGGGATCCCGAGGGTTCATCTCTTCCACGCTGTCTG	2587
QY	2581	CAGCCTGTGCTACGGGACATGAGAACAGCTGTGTCGGGGATTCGGCGGGACGGCT	2640
Db	2588	CAGCCTGTGCTACGGGACATGAGAACAGCTGTGTCGGGGATTCGGCGGGACGGCT	2647
QY	2641	GCTCCTGCGTTCGCTGATGATTTCTTGTGTCGACACCTCAGCTCACCCACCGGAAAC	2700
Db	2648	GCTCCTGCGTTCGCTGATGATTTCTTGTGTCGACACCTCAGCTCACCCACCGGAAAC	2707
QY	2701	CTTCTCAGAGACCTGCTGCGAGGTGCTCCTGATGATGCTGCTGCTGCTGCTGCTGCTG	2760
Db	2708	CTTCTCAGAGACCTGCTGCGAGGTGCTCCTGATGATGCTGCTGCTGCTGCTGCTGCTG	2767
QY	2761	GACAGTGGTGAACCTTCCCTGTAGAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2820
Db	2768	GACAGTGGTGAACCTTCCCTGTAGAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2827
QY	2821	GCGGCGCCAGGCTATTCCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2880
Db	2828	GCGGCGCCAGGCTATTCCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2887
QY	2881	GCAGAGGACTACTCAGCTATGCGCGGACCTCCATCAGAGCAGTCTCAGCTCAACCG	2940
Db	2888	GCAGAGGACTACTCAGCTATGCGCGGACCTCCATCAGAGCAGTCTCAGCTCAACCG	2947
QY	2941	CGCTTCAAGGCTGGAGAACATGCTGCTGCAAACTCTTTGGGCTCTTGGGCTGAGTG	3000
Db	2948	CGCTTCAAGGCTGGAGAACATGCTGCTGCAAACTCTTTGGGCTCTTGGGCTGAGTG	3007
QY	3001	TCACAGCCTCTTCTGGAATTCAGAGTGAACAGCCTCCAGACGCTGTCACCAACATCTA	3060
Db	3008	TCACAGCCTCTTCTGGAATTCAGAGTGAACAGCCTCCAGACGCTGTCACCAACATCTA	3067
QY	3061	CAAGATCTCTCTGCTGAGCGGTACAGGTTTTCAGGATGCTGCTGAGCTGCTGCTGCTGCTG	3120
Db	3068	CAAGATCTCTCTGCTGAGCGGTACAGGTTTTCAGGATGCTGCTGAGCTGCTGCTGCTGCTG	3127
QY	3121	TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGTCTCTCTGACACGCTGCTGCTGCTGCTG	3180
Db	3128	TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGTCTCTCTGACACGCTGCTGCTGCTGCTG	3187
QY	3181	CTGCTACTTCCATCTGAAAGCCCAAGAACGAGGATGCTGCTGCGGCGGAGGCGCGCG	3240
Db	3188	CTGCTACTTCCATCTGAAAGCCCAAGAACGAGGATGCTGCTGCGGCGGAGGCGCGCG	3247
QY	3241	GCGCCTCTCTCTGCTGAGCGGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
Db	3248	GCGCCTCTCTCTGCTGAGCGGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3307
QY	3301	GACTGCACACGCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3360
Db	3308	GACTGCACACGCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3367
QY	3361	GCTGAGTCGGAAGCTCCCGGGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3420
Db	3368	GCTGAGTCGGAAGCTCCCGGGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3427
QY	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGGGACTGATGGCCACCGCCGCCACAGCCGCGCA	3480

Db 3428 ACTCCCTCAGACTTCAAGACCACTCTGGACTGATGGCCACCCGCCACAGCCAGGCGGA 3487
Oy 3481 GAGCAGACACAGCAGCCCTGTACGCGGGCTCTACGTCCTCCAGGAGGAGGGCGGCC 3540
Db 3488 GAGCAGACACAGCAGCCCTGTACGCGGGCTCTACGTCCTCCAGGAGGAGGGCGGCC 3547
Oy 3541 CACACCCAGGCGCCACCGCTGGAGTCTGAGGCGCTGAGTGAGTGTGTTGGCCGAGGCGTG 3600
Db 3548 CACACCCAGGCGCCACCGCTGGAGTCTGAGGCGCTGAGTGAGTGTGTTGGCCGAGGCGTG 3607
Oy 3601 CATGTCGGCTGAAGGTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGCGCT 3660
Db 3608 CATGTCGGCTGAAGGTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGCGCT 3667
Oy 3661 GAGTGTCCAGCAGACACTTCCGCTCTTCACTTCCACAGGCTGGGCGCTCGGCTCCACCCCA 3720
Db 3668 GAGTGTCCAGCAGACACTTCCGCTCTTCACTTCCACAGGCTGGGCGCTCGGCTCCACCCCA 3727
Oy 3721 GGGCAGCTTTCTCACCAGGAGCGCGGCTTCCACTCCGCCACATAGAGATAGTCCATCC 3780
Db 3728 GGGCAGCTTTCTCACCAGGAGCGCGGCTTCCACTCCGCCACATAGAGATAGTCCATCC 3787
Oy 3781 CCAGATTCGCCATTTTCACCCCTCGCCCTGCGCTCTTGGCTTCCACCCACCATCC 3840
Db 3788 CCAGATTCGCCATTTTCACCCCTCGCCCTGCGCTCTTGGCTTCCACCCACCATCC 3847
Oy 3841 AGGTGGAGACCTTGAGAGGACCTTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
Db 3848 AGGTGGAGACCTTGAGAGGACCTTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3907
Oy 3901 CCCTGTACACAGGAGGACCTGCACCTGGATGGGGTCCCTGTGGTCAAAATGGGG 3960
Db 3908 CCCTGTACACAGGAGGACCTGCACCTGGATGGGGTCCCTGTGGTCAAAATGGGG 3967
Oy 3961 GAGTGTCTGGGAGTAAATACATATATAGTATTTTTCAGTATTTTGAATAAAA 4015
Db 3968 GAGTGTCTGGGAGTAAATACATATATAGTATTTTTCAGTATTTTGAATAAAA 4022

RESULT 9

ABL53711 standard; cDNA; 4070 BP.

XX ABL53711;

XX 17-JUN-2002 (first entry)

XX Human telomerase catalytic subunit hTERT cDNA.

XX hTERT; telomerase; reverse transcriptase; immortalisation; human;

XX vaccine; enzyme; gene; ss.

OS Homo sapiens.

PN WO200216555-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-GB03726.

XX 17-AUG-2000; 2000GB-0020246.

XX 17-AUG-2000; 2000US-225734P.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

XX Jones CJ, Kipling DG, Wilkinson G, McSharry B, Skinner JW;

XX WPI; 2002-315462/35.

XX Novel hTERT-immortalized cell line (human telomerase reverse
PT transcriptase) useful for human vaccine production and preparation of
PT antigen, such as a virus or virus-derived agent.

XX Example 1; Fig 1; 64pp; English.

XX The present sequence is that of hTERT cDNA in plasmid pGRN121.
CC hTERT is the catalytic subunit of human telomerase. Claimed
CC immortalised cell lines for use in vaccine production are adapted
CC to express hTERT. Suitable cell lines comprise human diploid
CC fibroblasts, e.g. MRC-5 or WI38 cells, transfected with hTERT cDNA
CC or infected by a retrovirus carrying hTERT cDNA, and are capable
CC of supporting antigen production. A method for preparing such cell
CC lines using recombinant techniques is provided. The cell lines
CC are also used as a diagnostic test for the presence of a virus
CC such as human cytomegalovirus, and to determine the efficacy of
CC antiviral agents by testing the capability of a modified virus
CC containing a reporter gene to infect the cells. The cell lines
CC have the ability, which can be impaired in cell lines immortalised
CC by other methods, of being able to support viral replication.
CC The cells remain morphologically suitable for viral/vaccine
CC cultivation.

XX SQ Sequence 4070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 other;

Query Match 100.0%; Score 4015; DB 24; Length 4070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGCGTCTGCTGTCGCGACGCTGGGAGAGCCCTGGCCCGGCCACCCCGCGATGCC 60

Db 21 GCAGCGTCTGCTGTCGCGACGCTGGGAGAGCCCTGGCCCGGCCACCCCGCGATGCC 80

Oy 61 GCGGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 120

Db 81 GCGGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 140

Oy 121 GCCCTGCGCACGCTTCGTCGCGGCGCTGGGCGCCCGAGGCTGGCGGTGTCAGCGCG 180

Db 141 GCCCTGCGCACGCTTCGTCGCGGCGCTGGGCGCCCGAGGCTGGCGGTGTCAGCGCG 200

Oy 181 GGACCCGGGCGCTTCCGCGGCGCTGCGCAGTGCCTGCTGCTGCGTGGCGTGGAGCG 240

Db 201 GGACCCGGGCGCTTCCGCGGCGCTGCGCAGTGCCTGCTGCTGCGTGGCGTGGAGCG 260

Oy 241 ACGGCGCGCGCGCGCGCGCGCGCTTCCCTCCGCGCAGGTGCTGCTGAAGAGCTGGTGG 300

Db 261 ACGGCGCGCGCGCGCGCGCGCGCTTCCCTCCGCGCAGGTGCTGCTGAAGAGCTGGTGG 320

Oy 301 CCGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGGCTTTCGCTTCGC 360

Db 321 CCGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGGCTTTCGCTTCGC 380

Oy 361 GCTGCTGGAGGGGCGCGCGCGCGCGCGCGCGCGCTTCCACACAGCGTGGCGAGCTA 420

Db 381 GCTGCTGGAGGGGCGCGCGCGCGCGCGCGCGCGCTTCCACACAGCGTGGCGAGCTA 440

Oy 421 CTGCCCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCTGGCTGCTGCTGCG 480

Db 441 CTGCCCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCTGGCTGCTGCTGCG 500

Oy 481 CCGGCTGGGCGACGAGCTGCTTACCTGCTGGCACGCTGCGCGCTCTTTTGTGCTGGT 540

Db 501 CCGGCTGGGCGACGAGCTGCTTACCTGCTGGCACGCTGCGCGCTCTTTTGTGCTGGT 560

Oy 541 GGCTCCAGCTGCGGCTTACAGGCTGCGGGGCGCGCGCGCTTACAGCTCGCGCTGGCAC 600

Db 561 GGCTCCAGCTGCGGCTTACAGGCTGCGGGGCGCGCGCGCTTACAGCTCGCGCTGGCAC 620

Oy 601 TCAGGCGCGCGCGCGCGCGCGCGCTAGTGGAGCCCGAGGCGCTGGGATCGCAACGGCG 660

Db 621 TCAGGCGCGCGCGCGCGCGCGCGCTAGTGGAGCCCGAGGCGCTGGGATCGCAACGGCG 680

Oy 661 CTGGAACCATAGCTCAGGAGGCGCGGGTCCCTGCGGCTGCGAGCCCGCGGTGCGAG 720

Db 681 CTGGAACCATAGCTCAGGAGGCGCGGGTCCCTGCGGCTGCGAGCCCGCGGTGCGAG 740

QY	721	GAGCGCGGGGCGAGTGCAGAGCCGAAGTCTGCCGTTGGCCAAAGAGAGCCGAGCGGTGGCG	780	1801	CAAGTTGCAAGCATTTGGAATCAGACAGACATTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
DB	741	GAGCGCGGGGCGAGTGCAGAGCCGAAGTCTGCCGTTGGCCAAAGAGAGCCGAGCGGTGGCG	800	1821	CAAGTTGCAAGCATTTGGAATCAGACAGACATTGAAGAGGGTGCAGCTCGGGAGCTGTC	1880
QY	781	TGCCCCCTGAGCGGAGCGGACGCCCTGTTGGGAGAGGGTCTCTGGGCCACCCGGGAGGAC	840	1861	GGAAGCAGAGGTCAGGACAGCATCGGAAGCCAGGCCGCCCTGCTGACGCTGCAGACTCCG	1920
DB	801	TGCCCCCTGAGCGGAGCGGACGCCCTGTTGGGAGAGGGTCTCTGGGCCACCCGGGAGGAC	860	1881	GGAAGCAGAGGTCAGGACAGCATCGGAAGCCAGGCCGCCCTGCTGACGCTGCAGACTCCG	1940
QY	841	GCGTGGACGAGTACCGGTGTTCTGTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGC	900	1921	CTTCATCCCAAGCCTGACGGCTCGCGCCGATTGTGTAAACATGGACTACGTCGTGGGAGC	1980
DB	861	GCGTGGACGAGTACCGGTGTTCTGTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGC	920	1941	CTTCATCCCAAGCCTGACGGCTCGCGCCGATTGTGTAAACATGGACTACGTCGTGGGAGC	2000
QY	901	CACCTCTTTGGAGGTTGCGCTCTGCGACGCGGCACCTCCACCCATCCGTTGGGCGGCA	960	1981	CAGAAGTTCGCCAGAGAAAGAGGCCCGAGCGTCTACCTCGAGGGTGAAGCACTGTT	2040
DB	921	CACCTCTTTGGAGGTTGCGCTCTGCGACGCGGCACCTCCACCCATCCGTTGGGCGGCA	980	2001	CAGAAGTTCGCCAGAGAAAGAGGCCCGAGCGTCTACCTCGAGGGTGAAGCACTGTT	2060
QY	961	GCACACAGCGGGCCCCCATCCACATCGGGGCCACACGCTCCCTGGGACACGCTTGTCC	1020	2041	CAGCGTCTCAACTACGAGCGGCGCGGCCCGGCTCCCTGGGCGCTCTGTCGTGGG	2100
DB	981	GCACACAGCGGGCCCCCATCCACATCGGGGCCACACGCTCCCTGGGACACGCTTGTCC	1040	2061	CAGCGTCTCAACTACGAGCGGCGGCGGCCCGGCTCTGTCGTGGG	2120
QY	1021	CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCTCAGCGACAAAGAGCAGCTGGG	1080	2101	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCTGCTGCTGTCGGGCCACAGACCC	2160
DB	1041	CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCTCAGCGACAAAGAGCAGCTGGG	1100	2121	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCTGCTGCTGTCGGGCCACAGACCC	2180
QY	1081	GCCCTCTCTACTCAGCTCTGTGAGGCCAGCCTGACTGGCGTTCGAGAGCTGTGGA	1140	2161	GCGCCTGAGCTGTACTTGTCAAGTGGATGTGACGGGCGGTACGACACCATCCCCCA	2220
DB	1101	GCCCTCTCTACTCAGCTCTGTGAGGCCAGCCTGACTGGCGTTCGAGAGCTGTGGA	1160	2181	GCGCCTGAGCTGTACTTGTCAAGTGGATGTGACGGGCGGTACGACACCATCCCCCA	2240
QY	1141	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT	1200	2221	GGACAGGCTCAGCGAGGTCTATCGCCAGCATCATCAAAACCCCAAGACACACTGCTGGG	2280
DB	1161	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT	1220	2241	GGACAGGCTCAGCGAGGTCTATCGCCAGCATCATCAAAACCCCAAGACACACTGCTGGG	2300
QY	1201	GCCCCAGCGCTACTGGCAATCGGCCCTGTTCTGAGCTGCTTGGAAACACAGCGCA	1260	2281	TGCGTATCGCGTGGTCCAGAGGCCGCCATGGGCAGCTCCGCAAGGCCCTTCAAGACCA	2340
DB	1221	GCCCCAGCGCTACTGGCAATCGGCCCTGTTCTGAGCTGCTTGGAAACACAGCGCA	1280	2301	TGCGTATCGCGTGGTCCAGAGGCCGCCATGGGCAGCTCCGCAAGGCCCTTCAAGACCA	2360
QY	1261	GTGCCCCCTACGGGTGCTCCTCAAGACGACTGCCGCTGCGAGCTGCGGTCAACCCAGC	1320	2341	CGTCTCTACTTGCACAGACTCCAGCGGTACATGCGACAGTTCGTCGCTCACTGCAGGA	2400
DB	1281	GTGCCCCCTACGGGTGCTCCTCAAGACGACTGCCGCTGCGAGCTGCGGTCAACCCAGC	1340	2361	CGTCTCTACTTGCACAGACTCCAGCGGTACATGCGACAGTTCGTCGCTCACTGCAGGA	2420
QY	1321	AGCCGCTGTCTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGGAGGAGGA	1380	2401	GACGACCGCTGAGGGATCGCGTCTCATCGACAGAGCTCCCTCCTGAATGAGGCCAG	2460
DB	1341	AGCCGCTGTCTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGGAGGAGGA	1400	2421	GACGACCGCTGAGGGATCGCGTCTCATCGACAGAGCTCCCTCCTGAATGAGGCCAG	2480
QY	1381	CACAGACCCCGTGGCTGGTGCAGTGTCTCGCCAGCACAGACGCCCCCTGCGAGTGA	1440	2461	CAGTGCCTCTTGCAGCTCTTCTACGCTTCATGTGCCACCGCGTGGCATCAGGGG	2520
DB	1401	CACAGACCCCGTGGCTGGTGCAGTGTCTCGCCAGCACAGACGCCCCCTGCGAGTGA	1460	2481	CAGTGCCTCTTGCAGCTCTTCTACGCTTCATGTGCCACCGCGTGGCATCAGGGG	2540
QY	1441	CGGCTTCGTGCGGGCTGCTTGGCGGGCTGGTGGCCCGGAGGCTCGGGCTCAGGCA	1500	2521	CAGTGCCTACGTCACGTCGCGAGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCG	2580
DB	1461	CGGCTTCGTGCGGGCTGCTTGGCGGGCTGGTGGCCCGGAGGCTCGGGCTCAGGCA	1520	2541	CAAGTCTACGTCACGTCGCGAGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCG	2600
QY	1501	CAACGAACCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAA	1560	2581	CAGCCTGTCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGACGGCT	2640
DB	1521	CAACGAACCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAA	1580	2601	CAGCCTGTCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGACGGCT	2660
QY	1561	GCTCTGCTGACAGGAGTGCAGTGGAGATGAGCGGTGCGGGACTCGCGTGGCTGCGGAG	1620	2641	GCTCTGCGTTCGTTGGTGGATGATTTCTGTGTGGTGACACCTTCACCTCACCCACGCAAAAC	2700
DB	1581	GCTCTGCTGACAGGAGTGCAGTGGAGATGAGCGGTGCGGGACTCGCGTGGCTGCGGAG	1640	2661	GCTCTGCGTTCGTTGGTGGATGATTTCTGTGTGGTGACACCTTCACCTCACCCACGCAAAAC	2720
QY	1621	GAGCCGAGGGTGGCTGTGTTCCGCGCCAGACACCGCTCTGCTGAGGAGATCTTGGC	1680	2701	CTTCCTCAGGACCCCTGGTCCGAGGTCTCCCTGAGTATGGCTGGTGAACCTTGGGAA	2760
DB	1641	GAGCCGAGGGTGGCTGTGTTCCGCGCCAGACACCGCTCTGCTGAGGAGATCTTGGC	1700	2721	CTTCCTCAGGACCCCTGGTCCGAGGTCTCCCTGAGTATGGCTGGTGAACCTTGGGAA	2780
QY	1681	CAAGTTCCTGCACTGGCTGATGTTGCTACGTCTGTCGAGCTGCTCAGGCTTTCTTTTA	1740	2761	GACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCACCGCTTTTCTCAGAT	2820
DB	1701	CAAGTTCCTGCACTGGCTGATGTTGCTACGTCTGTCGAGCTGCTCAGGCTTTCTTTTA	1760	2781	GACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCACCGCTTTTCTCAGAT	2840
QY	1741	TGTCAGGAGACACGCTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800	2821	GCGGCCACGCGCTATTCCCTTGGTGGCGCTGCTGCTGATACCCGACCCCTGGAGGT	2880
DB	1761	TGTCAGGAGACACGCTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1820	2841	GCGGCCACGCGCTATTCCCTTGGTGGCGCTGCTGCTGATACCCGACCCCTGGAGGT	2900
				2881	GCAGCGGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGCTCTACCTTCAACCG	2940

Db	2901	GCAGAGGACTACTCCAGCTATGCCGGAGCTCCATCAGAGCAGTCTCACCCTTCAACCG	2960
Qy	2941	CGGCTTCAAGGCTGGGAGGAACATGCTGCACAACTCTTTGGGTCTTGGGGTGAAGTG	3000
Db	2961	CGGCTTCAAGGCTGGGAGGAACATGCTGCACAACTCTTTGGGTCTTGGGGTGAAGTG	3020
Qy	3001	TCACAGCCTGTTTCTGGATTTCAGGTGAACAGGCTCCAGACGGTGTGCACCAACATCTA	3060
Db	3021	TCACAGCCTGTTTCTGGATTTCAGGTGAACAGGCTCCAGACGGTGTGCACCAACATCTA	3080
Qy	3061	CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGATGTGTGTCGAGCTCCCATTTCA	3120
Db	3081	CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGATGTGTGTCGAGCTCCCATTTCA	3140
Qy	3121	TCAGCAAGTTTGAAGAACCCACATTTTCTTCGCGGTCACTCTGACAGGGCTCCCT	3180
Db	3141	TCAGCAAGTTTGAAGAACCCACATTTTCTTCGCGGTCACTCTGACAGGGCTCCCT	3200
Qy	3181	CTGCTACTCCTCCTGAAAGCAAGAACGAGGATGTCGCTGGGGGCCAAGGGCGCGC	3240
Db	3201	CTGCTACTCCTCCTGAAAGCAAGAACGAGGATGTCGCTGGGGGCCAAGGGCGCGC	3260
Qy	3241	CGGCGCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACAAAGCATTCCTGTCAAGCT	3300
Db	3261	CGGCGCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACAAAGCATTCCTGTCAAGCT	3320
Qy	3301	GACTCGACACCGTGTCACTTAGCTGCCACTTCCTGGGTCACTCAGGACAGCCAGAGCGA	3360
Db	3321	GACTCGACACCGTGTCACTTAGCTGCCACTTCCTGGGTCACTCAGGACAGCCAGAGCGA	3380
Qy	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCCGACGCAACCCGGC	3420
Db	3381	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCCGACGCAACCCGGC	3440
Qy	3421	ACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGAGCCACCCGCCACAGCCGCGA	3480
Db	3441	ACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGAGCCACCCGCCACAGCCGCGA	3500
Qy	3481	GAGCAGACACGACAGCCCTGTACGCCGGCTCTACGTCCAGGGAGGAGGGCGGCGC	3540
Db	3501	GAGCAGACACGACAGCCCTGTACGCCGGCTCTACGTCCAGGGAGGAGGGCGGCGC	3560
Qy	3541	CACACCAGGCCCGCACCGCTGGAGTCTGAGGCCTGAGTGAGTGTGGCCGAGGCGTG	3600
Db	3561	CACACCAGGCCCGCACCGCTGGAGTCTGAGGCCTGAGTGAGTGTGGCCGAGGCGTG	3620
Qy	3601	CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCGTGAGCGAGTGTCCAGCCAAAGGCT	3660
Db	3621	CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCGTGAGCGAGTGTCCAGCCAAAGGCT	3680
Qy	3661	GAGTGTCCAGCACACCTCCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
Db	3681	GAGTGTCCAGCACACCTCCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3740
Qy	3721	GGGCCACCTTTTCTCACCAGGACCCCGGCTTCCACTTCCACATAGGAATAGTCTATCC	3780
Db	3741	GGGCCACCTTTTCTCACCAGGACCCCGGCTTCCACTTCCACATAGGAATAGTCTATCC	3800
Qy	3781	CCAGATTCGGCATTTGTTTACCCCTTCGCCCTCTCTTTGCCCTTCACCCCCACCATCC	3840
Db	3801	CCAGATTCGGCATTTGTTTACCCCTTCGCCCTCTCTTTGCCCTTCACCCCCACCATCC	3860
Qy	3841	AGTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAAATTGAGGTGACCAAAAGTGTG	3900
Db	3861	AGTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAAATTGAGGTGACCAAAAGTGTG	3920
Qy	3901	CCCTGTACAGGGAGGACCCCTGCACCTGGATGGGGTCCCTCTGGTCAAAATGGGG	3960
Db	3921	CCCTGTACAGGGAGGACCCCTGCACCTGGATGGGGTCCCTCTGGTCAAAATGGGG	3980
Qy	3961	GAGTGTCTGGGAGTAAAACTAGTAATATAGTATTTTTCAGTCTTTCAGAAAAA 4015	

Db	3981	GAGTGCTGGGAGTAAATACTGAATATATACGATTTTTCAGTTTGTGAAAAAAA
RESULT 10		
AAZ08150		
ID	AAZ08150	standard; cDNA; 4015 BP.
XX		
AC	AAZ08150;	
XX		
DT	17-JAN-2000	(first entry)
XX		
DE	Human telomerase reverse transcriptase cDNA.	
XX		
KW	Human telomerase reverse transcriptase; hTERT; telomerase; hEST2;	
KW	catalytic protein component; cell proliferative capacity;	
KW	cell immortality; neoplastic phenotype; diagnostic application;	
KW	prognostic application; telomerase related condition; cancer;	
KW	therapeutic agent; telomerase expression; telomerase activity; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	56..3454
FT		/*tag= a
FT		/product= "Human telomerase reverse transcriptase"
FT		/transl_except= (pos:1877..1879, aa:Gln)
XX		
PN	W09950279-A1.	
XX		
PD	07-OCT-1999.	
XX		
PF	31-MAR-1999;	99WO-US071160.
XX		
PR	31-MAR-1998;	98US-0052919.
XX		
PA	(GERO-) GERON CORP.	
PA	(UYTE-) UNIV TECHNOLOGY CORP.	
XX		
PI	Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley	
PI	Andrews WH;	
XX		
DR	WPI; 1999-610834/52.	
DR	P-PSDB; AAY28881.	
XX		
PT	Antisense polynucleotides for human telomerase reverse transcriptase	
PT	used for diagnosing or treating cancer -	
XX		
PS	Claim 1; Fig 1; 3lpp; English.	
XX		
CC	The present sequence encodes for human telomerase reverse transcriptase	
CC	(hTERT). This is the catalytic protein component of telomerase and	
CC	referred to as hEST2. This correlates with cell proliferative capacity	
CC	cell immortality, and the development of a neoplastic phenotype. H	
CC	TERT antisense oligonucleotides are useful for diagnostic or prognos	
CC	applications to telomerase related conditions, including cancer. T	
CC	also useful as therapeutic agents, for inhibition of telomerase	
CC	expression and activity.	
XX		
SO	Sequence 4015 BP; 563 A; 1364 C; 1274 G; 714 T; 0 other:	

Query Match	100.0%;	Score 4013.4;	DB 20;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4014;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
y	1	GCAGGCTGCTCTGCTGCGACCTGGGAGCCCTGCCCGCGCACCCCGCGATGCC	60	
b				
	1	GCAGGCTGCGTCTCTGCTGCGACCTGGGAGCCCTGCCCGCGCACCCCGCGATGCC	60	
y	61	GGCGCTCCCGCTGCCGAGCGCTGCTGCTGCGAGCCACATACCGCAGGTGCT	120	
b	61	GGCGCTCCCGCTGCCGAGCGCTGCTGCTGCTGCGAGCCACATACCGCAGGTGCT	120	
y	121	GGCGCTGGCCAGCTTGTGTCGGCGCTGCGGGGCCCGAGGGCTGGCGGGCTGGTGTGACGCGCGG	180	

QY	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATCCGACAGCTTCGTGCTCACCTGCAGGA	2400
Db	2341		2400
QY	2401	CGTCTCTACCTTGACAGACCTCCAGCCGTACATCCGACAGCTTCGTGCTCACCTGCAGGA	2400
Db	2401		2400
QY	2401	GACCAGCCCGCTGAGGGATCCGCTCGTCTCATCGACGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
Db	2401		2460
QY	2461	GACCAGCCCGCTGAGGGATCCGCTCGTCTCATCGACGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
Db	2461		2460
QY	2461	CAGTGGGCTCTTCGACGCTCTTCCTACGCTTCATGTCGCCACAGCCGTGCGCATCAGGG	2520
Db	2461		2520
QY	2521	CAAGTCTACGTCAGTGCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
Db	2521		2580
QY	2581	CAGCCTGTGTCACGGGACATGAGAACAAAGCTGTTTCGGGGATTCGGCGGACAGGGCT	2640
Db	2581		2640
QY	2641	GCCTCCGCTTGGTGGATGATTTCTGTTGGTGACACCTCACCTCACCCACACGCGAAAC	2700
Db	2641		2700
QY	2701	CTTCTCAGGACCTGGTCGAGGTGCCCTGAGTATGGCTGGTGGTGAACCTTGCGGAA	2760
Db	2701		2760
QY	2761	GACAGTGGTGAATTCCTCTAGAAGACGAGGCCCTGGTGGACGGCTTTTGTTCAGAT	2820
Db	2761		2820
QY	2821	GCGGGCCACGGCTATTTCCTGGTGGCGCCCTGCTGCTGAGTACCCGGACCCCTGGAGGT	2880
Db	2821		2880
QY	2881	GCAGAGGACTACTCCAGCTATCCGGAGCTCCATCAGACCGAGTCTCACCTTCAACCG	2940
Db	2881		2940
QY	2941	CGGCTTCAAGCTGGGAGAACATCGTCCGCAACTCTTTGGGGTCTTCGGGCTGAAGTG	3000
Db	2941		3000
QY	3001	TCACAGCCTGTTTCTGGATTGCAAGTGAACGCCCTCCAGACGGTGTGACCAACATCTA	3060
Db	3001		3060
QY	3061	CAAGATCTCTCTCTGAGGCGTACAGTTCACGATGTCGAGTCTCCAGTCCCATTTCA	3120
Db	3061		3120
QY	3121	TCAGCAAGTTTGAAGAACCCACATTTTTCCTGCGGTCATCTCTGACACGGCTCCCT	3180
Db	3121		3180
QY	3181	CTGCTACTCCATCCTTGAAGCCAAAGACGAGGGATGTGCTGGGGCCCAAGGGCGCCGC	3240
Db	3181		3240
QY	3241	CGGGCTCTGCCCTCCGAGGCCGTGAGTGGCTGTCGCCACCAAGATTCCTGCTCAAGCT	3300
Db	3241		3300
QY	3301	GACTCGACACCGTGTCACTTACCTGTCACCTCCCTGGGGTCACTCAGGACAGCCCGACGCA	3360
Db	3301		3360
QY	3361	GCTGAGTCGGAAGCTCCCGGGGACGAGCTGTACTGCCCTGGAGGCCGACGCCAACCCGC	3420
Db	3361		3420

QY	3421	ACTGCCCTCAGACTTCAAGACCATCTCGAGCTGATGCGCCACCGCCACAGCCAGGCCGA	3480
Db	3421	ACTCCCTCAGACTTCAAGACCATCTCGAGCTGATGCGCCACCGCCACAGCCAGGCCGA	3480
QY	3481	GAGCAGACACGAGCAGCCCTGTCACGCCGGGCTCTACGTCGCCAGGAGGAGGGGGCGCC	3540
Db	3481	GAGCAGACACGAGCAGCCCTGTCACGCCGGGCTCTACGTCGCCAGGAGGAGGGGGCGCC	3540
QY	3541	CACACCCAGGCCCCACCGCTGGAGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCGCTG	3600
Db	3541	CACACCCAGGCCCCACCGCTGGAGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCGCTG	3600
QY	3601	CATGTCGGGCTGAAGGCTGAGTGCCGGCTGAGGCCCTGAGCGAGTGCCAGCCAAAGGCT	3660
Db	3601	CATGTCGGGCTGAAGGCTGAGTGCCGGCTGAGGCCCTGAGCGAGTGCCAGCCAAAGGCT	3660
QY	3661	GAGTGTCAGCACACCTCCGCTCTTCACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA	3720
Db	3661	GAGTGTCAGCACACCTCCGCTCTTCACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA	3720
QY	3721	GGGCCAGCTTTTCCCTCACAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCCCTCACAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
QY	3781	CCAGATTGGCAATGTTACCCCTGCGGCTTCCACTCCCGCTCCATAGGAATAGTCCATCC	3840
Db	3781	CCAGATTGGCAATGTTACCCCTGCGGCTTCCACTCCCGCTCCATAGGAATAGTCCATCC	3840
QY	3841	AGGTGGAGACCCGTGAGAAGGACCTGGAGCTCTGGAAATTTGGAGTGACCAAGGTGTG	3900
Db	3841	AGGTGGAGACCCGTGAGAAGGACCTGGAGCTCTGGAAATTTGGAGTGACCAAGGTGTG	3900
QY	3901	CCCTGTACACAGCGGAGGCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960
Db	3901	CCCTGTACACAGCGGAGGCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960
QY	3961	GAGTGCTGTGGGAGTAAAAATACGTAATATATAGATTTTTCAGTTTTTGAAAAAA	4015
Db	3961	GAGTGCTGTGGGAGTAAAAATACGTAATATATAGATTTTTCAGTTTTTGAAAAAA	4015

RESULT 11

ABZ18391	
ID	ABZ18391 standard; cDNA; 4015 BP.
XX	
AC	ABZ18391;
XX	
DT	23-JAN-2003 (first entry)
XX	
DE	Group III cDNA cancer related clone SEQ ID NO:817.
XX	
KW	Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
KW	immune response; virology; immunology; microbiology; molecular biology;
KW	recombinant DNA technology; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200278516-A2.
XX	
PD	10-OCT-2002.
XX	
PF	28-MAR-2002; 2002WO-US10421.
XX	
PR	30-MAR-2001; 2001US-280255P.
PR	28-AUG-2001; 2001US-315563P.
PR	09-JAN-2002; 2002US-347313P.
XX	
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Wang T, Wang S, Bangur CS, Gaiger A;
XX	
DR	WPI; 2003-058387/05.
XX	

PT New immunogenic polynucleotides or polypeptides useful for diagnosing,
PT preventing and treating cancer expressing Ct or CP mRNA antigens, and
PT in virology, immunology, microbiology, molecular biology and
PT recombinant DNA techniques -
XX
XX
PS Claim 1; SEQ ID 817; 207pp; English.
XX
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytostatic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses Ct or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 4015 BP; 664 A; 1363 C; 1275 G; 713 T; 0 other;
Query Match 100.0%; Score 4013.4; DB 25; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAGCGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGCCGACACCCCGCGATGCC 60
DB 1 GCAGCGCTGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCGCCGACACCCCGCGATGCC 60
QY 61 GCGCGCTCCCGCTGCCGAGCGTGGCTCCCTGCTGCGACGCCACTACCGCGAGTGTCT 120
DB 61 GCGCGCTCCCGCTGCCGAGCGTGGCTCCCTGCTGCGACGCCACTACCGCGAGTGTCT 120
QY 121 GCCGTGGCCACGTTCTGCTGCGCGCTGGGGCCCGAGGCGTGGCGCTGGTGACGCGCG 180
DB 121 GCCGTGGCCACGTTCTGCTGCGCGCTGGGGCCCGAGGCGTGGCGCTGGTGACGCGCG 180
QY 181 GGAACCGGGGCTTCCCGCGCGCTGGTGCCCGAGTGGCTGGCTGCGCTTGGCTTCCG 240
DB 181 GGAACCGGGGCTTCCCGCGCGCTGGTGCCCGAGTGGCTGGCTGCGCTTGGCTTCCG 240
QY 241 ACGGGCGCCCGCGCGCCCTCTCTCCGCGAGGTGCTCTGCTGAAGAGTGTGTGGC 300
DB 241 ACGGGCGCCCGCGCGCCCTCTCTCTCCGCGAGGTGCTCTGCTGAAGAGTGTGTGGC 300
QY 301 CCGAGTGTGTGAGAGCTGTGCGAGCGCGCGCGCGAAGACGTGCTGGCTTGGCTTCCG 360
DB 301 CCGAGTGTGTGAGAGCTGTGCGAGCGCGCGCGCGAAGACGTGCTGGCTTGGCTTCCG 360
QY 361 GCTGTGGACGGGGCGCGGGGGCCCGCCCGAGGCGTTCACACAGCGTGGCGAGCTA 420
DB 361 GCTGTGGACGGGGCGCGGGGGCCCGCCCGAGGCGTTCACACAGCGTGGCGAGCTA 420
QY 421 CTGTCCCAACAGGTGACCGAGCGACTGCGGGGAGCGGGGCTGCTGCTGCG 480
DB 421 CTGTCCCAACAGGTGACCGAGCGACTGCGGGGAGCGGGGCTGCTGCTGCG 480
QY 481 CCGCGTGGCGACGAGCTGCTGCTTACCTGCTGCGACGCTGCGGCTCTTGTGCTGT 540
DB 481 CCGCGTGGCGACGAGCTGCTGCTTACCTGCTGCGACGCTGCGGCTCTTGTGCTGT 540
QY 541 GCGTCCAGCTGCGGCTACCAAGTGTGGGGCGCGCGTGTACAGCTGCGGCTGCCAC 600
DB 541 GCGTCCAGCTGCGGCTACCAAGTGTGGGGCGCGCGTGTACAGCTGCGGCTGCCAC 600
QY 601 TCAGCGCGGGCCCGCCACAGCTAGTGGACCCCGAGGCGCTCTGGGATGCGAGCGGC 660
DB 601 TCAGCGCGGGCCCGCCACAGCTAGTGGACCCCGAGGCGCTCTGGGATGCGAGCGGC 660
QY 661 CTGGAACCATAGCTGTCAGGAGCGCGGGTCCCTGCGGCTGCCAGCCCGGGTGCAG 720
DB 661 CTGGAACCATAGCTGTCAGGAGCGCGGGTCCCTGCGGCTGCCAGCCCGGGTGCAG 720

QY 721 GAGGCGCGGGGACGTGCCAGCGGAAGTCTGCCGTTGGCCAAAGAGCCCGAGCGGTGGCG 780
DB 721 GAGGCGCGGGGACGTGCCAGCGGAAGTCTGCCGTTGGCCAAAGAGCCCGAGCGGTGGCG 780
QY 781 TGGCCCTGAGCGGGAGCGGACGCCCTTGGGCAGGGGTCTTGGGCGCCACCCGGGCGAGAC 840
DB 781 TGGCCCTGAGCGGGAGCGGACGCCCTTGGGCAGGGGTCTTGGGCGCCACCCGGGCGAGAC 840
QY 841 GCGTGACCGAGTACCGTGGTTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GCGTGACCGAGTACCGTGGTTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 CACCTCTTTGGAGGTGCGCTCTGTGGCAGCGGCCACTCCACCCATCTCCACCCATCTCC 960
DB 901 CACCTCTTTGGAGGTGCGCTCTGTGGCAGCGGCCACTCCACCCATCTCCACCCATCTCC 960
QY 961 GCACCAAGCGGGCCCGCCGATCCACATCGCGGCCACCCAGCTCTCTGGACACGCTTGTCC 1020
DB 961 GCACCAAGCGGGCCCGCCGATCCACATCGCGGCCACCCAGCTCTCTGGACACGCTTGTCC 1020
QY 1021 CCGGCTGTACGCGGAGACCAAGCACCTTCTACTCTCTACTCAGGCGCAAGGAGCAGCTGCG 1080
DB 1021 CCGGCTGTACGCGGAGACCAAGCACCTTCTACTCTCTACTCAGGCGCAAGGAGCAGCTGCG 1080
QY 1081 GCGCTCTTCTACTCTGTAGGCCAGCCTGTACTGTGGGCTTCGAGGCTTCGTGGA 1140
DB 1081 GCGCTCTTCTACTCTGTAGGCCAGCCTGTACTGTGGGCTTCGAGGCTTCGTGGA 1140
QY 1141 GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTTCCCGCAGGTTGCCCGCGCT 1200
DB 1141 GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTTCCCGCAGGTTGCCCGCGCT 1200
QY 1201 GCGCCAGCGCTACTGTGCAAAATGCGGCCCTCTTCTGTGAGCTGCTTGGAAACACACGCGA 1260
DB 1201 GCGCCAGCGCTACTGTGCAAAATGCGGCCCTCTTCTGTGAGCTGCTTGGAAACACACGCGA 1260
QY 1261 GTGCCCCCTACGGGGTCTCTCAAGACGACACTGCCCGCTCGAGCTGCGGTTCACCCAGC 1320
DB 1261 GTGCCCCCTACGGGGTCTCTCAAGACGACACTGCCCGCTCGAGCTGCGGTTCACCCAGC 1320
QY 1321 AGCGGCTGTGTGCGCGGAGAACCCAGAGGCTCTGTGGCGGCCCGCGAGGAGGA 1380
DB 1321 AGCGGCTGTGTGCGCGGAGAACCCAGAGGCTCTGTGGCGGCCCGCGAGGAGGA 1380
QY 1381 CACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGCCAGCAGCAGAGCCCTTGGCAGTGT 1440
DB 1381 CACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGCCAGCAGCAGAGCCCTTGGCAGTGT 1440
QY 1441 CCGCTTGTGCGGGGCTGCTGCGCGGCTGCTGCGCGGCTGCTGCGCGGCTTGGGCTTCCAG 1500
DB 1441 CCGCTTGTGCGGGGCTGCTGCGCGGCTGCTGCGCGGCTGCTGCGCGGCTTGGGCTTCCAG 1500
QY 1501 CAACGAACCGCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA 1560
DB 1501 CAACGAACCGCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA 1560
QY 1561 GCTCTGCTGCGAGGCTGACCTGGAAGATGAGCGTGCAGGCTGCGCTTGGTGGCGAG 1620
DB 1561 GCTCTGCTGCGAGGCTGACCTGGAAGATGAGCGTGCAGGCTGCGCTTGGTGGCGAG 1620
QY 1621 GAGCCCGAGGGTGGCTGTTCGCGCGCGAGACAGCTCTCGCTGAGGAGTCTCTGGC 1680
DB 1621 GAGCCCGAGGGTGGCTGTTCGCGCGCGAGACAGCTCTCGCTGAGGAGTCTCTGGC 1680
QY 1681 CAAGTTCCTGCACTGCTGATGAGTGTACGCTGCTGAGCTCTCTTCTTTT 1740
DB 1681 CAAGTTCCTGCACTGCTGATGAGTGTACGCTGCTGAGCTCTCTTCTTTT 1740
QY 1741 TGTCCAGGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG 1800
DB 1741 TGTCCAGGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG 1800

QY 1801 CAAGTTCGAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGTC 1860
Db 1801 CAAGTTCGAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGTC 1860
QY 1861 GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG 1920
Db 1861 GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG 1920
QY 1921 CTTTCATCCCAAGCCTGACGGGCTGCGCGGATGTTGAATGAGTACGTCTGCGGAGC 1980
Db 1921 CTTTCATCCCAAGCCTGACGGGCTGCGCGGATGTTGAATGAGTACGTCTGCGGAGC 1980
QY 1981 CAGAACCTTCGCGAGAGAAAGAGCGCGGCGCTTCACTCGAGGCTGAAGGCACTGTT 2040
Db 1981 CAGAACCTTCGCGAGAGAAAGAGCGCGGCGCTTCACTCGAGGCTGAAGGCACTGTT 2040
QY 2041 CAGCGTCTCAACTACGAGGGGCGCGCGGCGCTTCACTCGAGGCTTCTGTCGCTGGG 2100
Db 2041 CAGCGTCTCAACTACGAGGGGCGCGCGGCGCTTCACTCGAGGCTTCTGTCGCTGGG 2100
QY 2101 CTTGGAGATATCCACAGGGGCTGGCGCACTTCTGCTGCTGGGTGTGCGGGCCAGGACCC 2160
Db 2101 CTTGGAGATATCCACAGGGGCTGGCGCACTTCTGCTGCTGGGTGTGCGGGCCAGGACCC 2160
QY 2161 GCCGCTGAGTGTACTTGTCAAGGTGGATGTACGGGGCGGTACGACACCATCCGCCA 2220
Db 2161 GCCGCTGAGTGTACTTGTCAAGGTGGATGTACGGGGCGGTACGACACCATCCGCCA 2220
QY 2221 GGACAGGCTCACGGAGTCTATCGCAGCATCATCAAAACCCAGAACACGTCTGCTGCG 2280
Db 2221 GGACAGGCTCACGGAGTCTATCGCAGCATCATCAAAACCCAGAACACGTCTGCTGCG 2280
QY 2281 TCGGTATGCGGTGTCAGAGGCGCGCCATGCGGACGTGCGCAAGGCCCTTCAAGAGCCA 2340
Db 2281 TCGGTATGCGGTGTCAGAGGCGCGCCATGCGGACGTGCGCAAGGCCCTTCAAGAGCCA 2340
QY 2341 CGTCTCTACCTTGACAGCTTCCAGCGGTATCATGCGAGTTCGTCGCTCACCCTGCAGGA 2400
Db 2341 CGTCTCTACCTTGACAGCTTCCAGCGGTATCATGCGAGTTCGTCGCTCACCCTGCAGGA 2400
QY 2401 GACCAGCCCGTGAGGGATCCGCTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
Db 2401 GACCAGCCCGTGAGGGATCCGCTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
QY 2461 CAGTGGGCTCTTCAGCTCTTCTACGCTTCATGCTGTCACACGCCGTGGCATCAGGGG 2520
Db 2461 CAGTGGGCTCTTCAGCTCTTCTACGCTTCATGCTGTCACACGCCGTGGCATCAGGGG 2520
QY 2521 CAAGTCTCTACGTCAGTCCAGGGATCCCGCAGGGCTCCATCTCTCCAGGCTGCTCTG 2580
Db 2521 CAAGTCTCTACGTCAGTCCAGGGATCCCGCAGGGCTCCATCTCTCCAGGCTGCTCTG 2580
QY 2581 CAGCCTGTGCTACGGCGACATGGAGAAAGCTTTTTCGGGGATTCGGGGGACGGCT 2640
Db 2581 CAGCCTGTGCTACGGCGACATGGAGAAAGCTTTTTCGGGGATTCGGGGGACGGCT 2640
QY 2641 GTCCTCGGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGGGAAAC 2700
Db 2641 GTCCTCGGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGGGAAAC 2700
QY 2701 CTTCTCTCAGGACCTGTGTCAGAGTGTCCCTGAGTATGGCTGCTGCTGAGTTCGGGAA 2760
Db 2701 CTTCTCTCAGGACCTGTGTCAGAGTGTCCCTGAGTATGGCTGCTGCTGAGTTCGGGAA 2760
QY 2761 GACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
Db 2761 GACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
QY 2821 GCGGGCCACGGCCCTATTCCTCGGTGCGGCTGCTGCTGATACCCGACCCCTGGAGGT 2880
Db 2821 GCGGGCCACGGCCCTATTCCTCGGTGCGGCTGCTGCTGATACCCGACCCCTGGAGGT 2880
QY 2881 GCAGAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940

Db 2881 GCAGAGGCACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2941 CGGCTTCAAGGCTGGGAGGAACATGCTGCGAAACTCTTTGGGCTCTTTGGGCTGAAGTG 3000
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCTGCGAAACTCTTTGGGCTCTTTGGGCTGAAGTG 3000
QY 3001 TCACAGGCTGTTCCTGATTTGAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
Db 3001 TCACAGGCTGTTCCTGATTTGAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
QY 3061 CAGATCTCTGCTGTCAGGGCTACAGTTTTCAGGCATGTGCTGCTCAGCTCCCATTTCA 3120
Db 3061 CAGATCTCTGCTGTCAGGGCTACAGTTTTCAGGCATGTGCTGCTCAGCTCCCATTTCA 3120
QY 3121 TCACAAAGTTTGAAGAAACCCACATTTTCTCGGCTCATCTCTGACAGGGCTCCCT 3180
Db 3121 TCACAAAGTTTGAAGAAACCCACATTTTCTCGGCTCATCTCTGACAGGGCTCCCT 3180
QY 3181 CTGCTACTCTCACTTGAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCGCGC 3240
Db 3181 CTGCTACTCTCACTTGAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCGCGC 3240
QY 3241 CGGCCCTCTGCCCTCCAGGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Db 3241 CGGCCCTCTGCCCTCCAGGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
QY 3301 GACTCGACACCGCTGCTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Db 3301 GACTCGACACCGCTGCTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
QY 3361 GCTGAGTGGGAAGTCCCGGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Db 3361 GCTGAGTGGGAAGTCCCGGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
QY 3421 ACTGCCCTCAGACTTCAAGACCACTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Db 3421 ACTGCCCTCAGACTTCAAGACCACTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3481 GAGCAGACACCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3481 GAGCAGACACCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
QY 3541 CACACCCAGGCGCCACCGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 3600
Db 3541 CACACCCAGGCGCCACCGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 3600
QY 3601 CATGTCGGCTGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 CATGTCGGCTGAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3661 GAGTGTCCAGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Db 3661 GAGTGTCCAGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
QY 3721 GGGCCAGCTTTTCTCACCAGGAGCCGCTTCCACTCCACATAGGAATAGTCCATCC 3780
Db 3721 GGGCCAGCTTTTCTCACCAGGAGCCGCTTCCACTCCACATAGGAATAGTCCATCC 3780
QY 3781 CCAGATTCGCAATTTTCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
Db 3781 CCAGATTCGCAATTTTCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
QY 3841 AGGTGGAGACCTTGAGAGGACCTTGGGAGCTTGGGAATTTGAGTGTGACCAAGGTGTG 3900
Db 3841 AGGTGGAGACCTTGAGAGGACCTTGGGAGCTTGGGAATTTGAGTGTGACCAAGGTGTG 3900
QY 3901 CCCTGTACAGAGGAGGACCCCTGCACTGATGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
Db 3901 CCCTGTACAGAGGAGGACCCCTGCACTGATGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
QY 3961 GAGTGTGCTGGGAGTAAATACTGATATATGATTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTT 4015

Db 1204 G C C C A G C G T A C T G G C A A A T G C G G C C C T G T T T C T G G A G C T G T T G G A A C C A C G C G C A 1263
Qy 1261 G T G C C C C T A C G G G T G T C C T C A A G A G C A C T G C C G C T G C G A C T G C G G T C A C C C C A G C 1320
Db 1264 G T G C C C C T A C G G G T G T C C T C A A G A G C A C T G C C G C T G C G A C T G G G T C A C C C C A G C 1323
Qy 1321 A G C C G G T G T G T G C C C G G G A A G C C C A G G G C T G T G T G C G C C C C C G A G G A G A G A 1380
Db 1324 A G C C G G T G T G T G C C C G G G A A G C C C A G G G C T G T G T G C G C C C C C G A G G A G A G A 1383
Qy 1381 C A C A G A C C C G C T G C C T G T G C A G C T G C C G C C A C A G C A C A G C C C T G C G C A G T G T A 1440
Db 1384 C A C A G A C C C G C T G C C T G T G T G C A G C T G C C G C C A C A G C A G C C C T G G C A G T G T A 1443
Qy 1441 C G G C T T G T G C G G G C C T G C C T G C C G C G C T G G T G C C C C A G G C C T C T G G G C T C C A G G C A 1500
Db 1444 C G G C T T G T G C G G G C C T G C C T G C C G C G C T G T G C C C C A G G C C T C T G G G C T C C A G G C A 1503
Qy 1501 C A A C A A G C C G C T T C C T C A G G A A C A C A A G A T T C A T C T C C T G G G G A A G C A T G C C A A 1560
Db 1504 C A A C A A G C C G C T T C C T C A G A A A C A C C A A G A T T C A T C T C C C T G G G A A G C A T G C C A A 1563
Qy 1561 G C T C T G C T G C A G A G C T G A G T G G A A G A T G A G C T G C G G A C T G C G C T G G C T G C G C A G 1620
Db 1564 G C T C T G C T G C A G A G C T G A G T G G A A G A T G A G C T G C G G G C T G C G C T T G G C T G C G C A G 1623
Qy 1621 G A G C C C A G G G T T G G C T G T G T C C G G C C G C A G A C C C G T G C G T G A G G A G A T C C T G G C 1680
Db 1624 G A G C C C A G G G T T G G C T G T G T C C G C C G C A G A C C C G T G C G T G A G G A G A T C C T G G C 1683
Qy 1681 C A A G T T C T G C A C T G G C T G A T G A T G T G A C T G T G A G C T G C T A G G C T G C T T C T T T T A 1740
Db 1684 C A A G T T C T G C A C T G G C T G A T G A T G T G A C T G T G A G C T G C T A G G C T G C T T C T T T T A 1743
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Db 1804 C A A G T T G A A A G A T T G A A T C A G A C A C A T T G A A G A G G T G A G C T G C G G G A G C T G T C 1863
Qy 1861 G G A G C A G A G T C A G G A G C A T C G G A G C C G C C C C C T G C T A G G T C C A C A C T C C G 1920
Db 1864 G G A G C A G A G T C A G G A G C A T C G G A G C C A G C C C C C C T G C T A G C T C C A G A C T C C G 1923
Qy 1921 C T T C A T C C C A A G C T C A C G G C T C C G G C C G A T T G T G A A C A T G G A C T A C G T C G T G G A G C 1980
Db 1924 C T T C A T C C C A A G C T G A C G G C T G C G C C G A T T G T G A A C A T G G A C T A C G T C G T G G A G C 1983
Qy 1981 C A G A A C G T T C C G C A G A A A A G A G G C C G A G G C T C A C C T C G A G G G T G A A G C A C T G T T 2040
Db 1984 C A G A A C G T T C C G C A G A A A A A G A G G C C G A G C G T C A C C T C G A G G G T G A A G C A C T G T T 2043
Qy 2041 C A G C G T G C T A A C T A C A G A G G C C G C G C C C C C C C C C C T C C T G G C G C C T G T G C T G G G 2100
Db 2044 C A G C G T G C T A A C T A C A G A G G C C G C G C C C C C C C C C C C C C C C C C C T C T G T G C T G G G 2103
Qy 2101 C C T G A C A T A T C C A C A G G G C T G C G C A C C T T C G T G C G T G T G C G G G C C C A G G A C C C 2160
Db 2104 C C T G A C A T A T C C A C A G G G C T G C G C A C C T T C G T G C G T G T G C G G G C C C A G G A C C C 2163
Qy 2161 G C C G C C T A G C T G A C T T T G T C A A G T G G A T G T G A C G G G C G C T A C G A C A C C A T C C C C C A 2220
Db 2164 G C C G C C T A G C T G A C T T T G T C A A G T G G A T G T G A C G G G C G C T A C G A C A C A T C C C C C A 2223
Qy 2221 G G A C A G C T C A C G A G G T C A T C G C A G C A T C A A A C C C C A G A A C A C A G T A C T C G T G C G 2280
Db 2224 G G A C A G C T C A C G A G G T C A T C G C A G C A T C A A A C C C C A G A A C A C A G T A C T C G T G C G 2283
Qy 2281 T C G T A T C C C T G T T C C A A A G G C C C C A T G G C A C G T C C G A A G C C T T C A A G A G C A 2340

Db 2284 T C G T A T C C C G T G T C C A A A G C C C C C A T G G C A C G T C G C A A G C C C T T C A A G A G C C A 2343
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Qy 2401 G A C C A G C C C C T G A G G A T G C C T G C G T A T C G A C C A G A G C T C C C C T G A T G A G G C C A G 2460
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Qy 2461 C A G T G G C C T T C T G A C G T C T T C T A C G T T A T G T G C C A C A C A C C C G T G C G C A T C A C A G G G 2520
Db 2464 C A G T G G C C T T C T G A C G C T T C C T A C C G T T A T G T G C C A C A C C C C G T G C G C A T C A G G G 2523
Qy 2521 C A A G T C C T A C G T C C A G T C C C A G G G A T C C C G C A G G G T C C A T C C T C C A C G C T G C T G 2580
Db 2524 C A A G T C C T A C G T C C A G T C C C A G G G A T C C C G C A G G G T C C A T C C T C C A C G C T G C T G 2583
Qy 2581 C A G C C T G T G T A C G G C A C A T G G A A A C A A G C T G T T T G C G G G A T T C G G C G G A C G G C T 2640
Db 2584 C A G C C T G T G T A C G G C A C A T G G A A A C A A G C T G T T T G C G G G A T T C G G C G G A C G G C T 2643
Qy 2641 G C T C C T G C T T T G T G A T G A T T T C T T T G T T G T G A C A C C T C A C C T C A C C A C G C G A A A A C 2700
Db 2644 G C T C C T G C T T T G T G A T G A T T T C T T T G T T G T G A C A C C T C A C C T C A C C A C G C G A A A A C 2703
Qy 2701 C T T C C T C A G A C C C T G T C C G A G T G T C C C T A G T A T G G T G C T G T G T G A A C T T G C G A A 2760
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Qy 2761 G A C A G T G T G A A C T T C C C T G T A G A A G A G A G G C C C T G G T G G C A C G C T T T G T T C A G A T 2820
Db 2764 G A C A G T G T G A A C T T C C C T G T A G A A G A G A G G C C C T G G T G G C A C G C T T T T G T T C A G A T 2823
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Qy 3301 G A C T C G A C A C C G T C A C C T A C T G C C A C T C C T G G G G T C A C T C A G G A C A G C C C A G A G C A 3360
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Db 3604 CATGTCCGCTGAGGCTGAGTGTCCGCGCTGAGGCTGAGCGAGTGTCCAGCCAGGGCT 3663
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Db 3844 AGGTGAGACCTCTGAGAGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAAAGTGTG 3903
QY 3901 CCTGTACACAGCGAGACCTGACCTGAGTGGGGTCCCTGTGGGTCAAAATGGGGG 3960
Db 3904 CCTGTACACAGCGAGACCTGACCTGAGTGGGGTCCCTGTGGGTCAAAATGGGGG 3963
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Db 3964 GAGGTGCTGTGGAGTAAATACTGAATATAGTGTTCAGTTTGAATAAAA 4018
```

RESULT 13

AAV22428
ID AAV22428 standard; cDNA; 4037 BP.
XX
AC AAV22428;

13-AUG-1998 (first entry)

Human telomerase reverse transcriptase encoding cDNA refined sequence.

Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 56..3454
/*tag= a
/product= "telomerase reverse transcriptase"
/note= "refined sequence"

GB2317891-A.

08-APR-1998.

01-OCT-1997; 97GB-0020890.

14-AUG-1997; 97US-0915503.

01-OCT-1996; 96US-0724643.

18-APR-1997; 97US-0844419.

25-APR-1997; 97US-0846017.

PR

06-MAY-1997; 97US-0851843.

PR 09-MAY-1997; 97US-0854050.

PR 14-AUG-1997; 97US-0911312.

PR 14-AUG-1997; 97US-0912951.

XX

(GERO-) GERON CORP.

(UYTE-) UNIV TECHNOLOGY CORP.

PA

Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;

PI

Morin GB, Nakamura T, Harley CB;

XX

WPI; 1998-171633/16.

DR

P-PSDB; AAW56113.

XX

Pure and recombinant human Telomerase Reverse Transcriptase and its

PT

variants - are useful in the diagnosis, prognosis and treatment of

PT

cell proliferation conditions especially cancer and ageing

XX

Example 1; Fig 74; 387pp; English.

XX

The present sequence encodes human telomerase reverse transcriptase (hTERT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein with the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods.

SQ Sequence 4037 BP; 682 A; 1362 C; 1275 G; 714 T; 4 other;

Query Match 99.8%; Score 4007; DB 19; Length 4037;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4007; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Db 61 GCGCGTCCCGCTGCGCGACGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGCT 120

QY 121 GCGCGTGGCCACGTTGCTGGGGCGCTGGGGCCCCAGGGCTGGGGCTGGTGGAGCGCG 180

Db 121 GCGCGTGGCCACGTTGCTGGGGCGCTGGGGCCCCAGGGCTGGGGCTGGTGGAGCGCG 180

QY 181 GGACCCGGCGGCTTCCGGCGCTGGTGGCCCGCTGGTGGCTGGCTGGCTGGCTGGCTGG 240

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Db 241 ACGGCGCGCGCGCGCGCGCGCGCTTCCCTTCCGCGCCAGGTGTCTGCTCTGAAGAGCTGGTGGC 300

QY 301 CCGAGTGTGTGAGAGGCTGTGCGAGCGCGCGCGGAGAAACGTGCTGCGCTTCGGCTTCGC 360

Db 301 CCGAGTGTGTGAGAGGCTGTGCGAGCGCGCGGAGAAACGTGCTGCGCTTCGGCTTCGC 360

QY 361 GCTGTGGACGGGGCGGG 420

Db 361 GCTGTGGACGGGGCGGG 420

Db 361 GCTGCTGGACGGGGCCCCGGGGGCCCCCGAGGCCCTTACACACAGCGTGGCCAGCTA 420
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Db 421 CCTGCCCAACACAGGTGACCGACGACATGCGGGGAGCGGGGCGTGGCTGCTGCTGG 480
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Db 481 CCGCGTGGGGACACAGTGTCTGTTACCTGCTGGCAGCGTGGCGGCTCTTTGTGCTGGT 540
Qy 541 GGCTCCACAGTGGCCCTACACAGGTGTGGGGCCCGCTGTACACAGTGGCGCTGCCAC 600
Db 541 GGCTCCACAGTGGCCCTACACAGGTGTGGGGCCCGCTGTACACAGTGGCGCTGCCAC 600
Qy 601 TCAGGCCGGCCCCCGCCACACAGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGC 660
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Qy 661 CTGGAACCATAGCTCAGGAGGCGGGGTGCCCTGGGCGTGGCAGCCCGGGTGGGAG 720
Db 661 CTGGAACCATAGCTCAGGAGGCGGGGTGCCCTGGGCGTGGCAGCCCGGGTGGGAG 720
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Db 721 GAGCGCGGGGAGTGCACAGCAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGGCG 780
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Db 841 GCGTGGACCGAGTACCGTGGTTCCTGTTGTTGCTGACCTGCGCAGACCCCGCGAAGAC 900
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Db 2521 CAAGTCTCTAGCTCCAGTGGCAGGGATCCCGCAGGGTCCATCTCTCCAGGCTGCTG 2580

progenitor cells in in vivo, in vitro or ex vivo protocols. The methods can be used for promoting the healing of wounds resulting from e.g. surgery, burns, inflammation or irritation or ulcers resulting from e.g. venous disease (venous stasis ulcers), excessive pressure (decubitus ulcers) or arterial ulcers. They can also be used to enhance tissue regeneration processes, e.g. of the skin, hair and/or fingernails. They can also be used for treating age-related conditions, e.g. atrophy of the skin through loss of extracellular matrix homeostasis in dermal fibroblasts, age-related macular degeneration caused by accumulation of lipofuscin and downregulation of a neuronal survival factor in retinal pigmented epithelial (RPE) cells, and atherosclerosis caused by loss of proliferative capacity and overexpression of hypertensive and thrombotic factors in endothelial cells. Expanded populations of normal or genetically engineered rejuvenated cells could be used for autologous or allogeneic cell and gene therapy. They can also be used for prolonging the lifespan of a culture of normal cells or tissue being used to secrete therapeutic or other commercially significant proteins and products.

SQ Sequence 4027 BP; 674 A; 1361 C; 1277 G; 715 T; 0 other;

Query Match 99.7%; Score 4002; DB 20; Length 4027;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4005; Conservative 0; Mismatches 5; Indels 0;

Qy	6	GCTCGCTCTGCTGCGACGTGGGAAGCCCTTGCCCCCGGCACACCCCGCATGCGCGCG	65
Db	7		66
		GCGTGGTCTCTGCTGCGACGTGGGAAGCCCTTGCCCCCGGCACACCCCGCATGCGCGCG	
Qy	66	CTCCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGCAGCACCTACCGCGAGTGTGTCGCG	125
Db	67		126
		CTCCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGCAGCACCTACCGCGAGTGTGTCGCG	
Qy	126	TGGCCACGTTCTGTCGGCGCGCTGGGGCCCCACAGGGCTGGTGGCAGCGCGGGGACC	185
Db	127		186
		TGGCCACGTTCTGTCGGCGCGCTGGGGCCCCAGGGCTGGTGGCAGCGCGGGGACC	
Qy	186	CGGGGCTTTCCGGCGCGTGTGTGCGCAGTGCCTTGGTGTGCGTGCCTTGGACGCACGCG	245
Db	187		246
		CGGGGCTTTCCGGCGCGTGTGTGCGCAGTGCCTTGGTGTGCGTGCCTTGGACGCACGCG	
Qy	246	CGCCCCCGCGCCCTCTCTTCGCGCAGGTGTCTTGCTTAAGGAGCTGTGTGCCCCAG	305
Db	247		306
		CGCCCCCGCGCCCTCTCTTCGCGCAGGTGTCTTGCTTAAGGAGCTGTGTGCCCCAG	
Qy	306	TGCTGCAAGAGCTGTGGGAGCGCGCGGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGC	365
Db	307		366
		TGCTGCAAGAGCTGTGGGAGCGCGCGGAAGAACGTGCTGGCCTTCGCGCTGC	
Qy	366	TGGACGGGGCGCGGGGGCCCCCGGAGGCTTCAACACAGCGTGGCGAGCTACCTGC	425
Db	367		426
		TGGACGGGGCGCGGGGGCCCCCGGAGGCTTCAACACAGCGTGGCGAGCTACCTGC	
Qy	426	CCAAACGGTGCACGACGCTGTCGGGGAGCGGGGCTGGGGGCTGCTGCTGGCGCGCG	485
Db	427		486
		CCAAACGGTGCACGACGCTGTCGGGGAGCGGGGCTGGGGGCTGCTGCTGGCGCGCG	
Qy	486	TGGCGCAGCAGTGTCTGTTTACCTGCTGGCAGCCTGCGCGCTCTTTGCTGTTGGGCTC	545
Db	487		546
		TGGCGCAGCAGTGTCTGTTTACCTGCTGGCAGCCTGCGCGCTCTTTGCTGTTGGGCTC	
Qy	546	CCAGCTCGGCTACCAAGTGTGGGGCGCGGCTGTATCCAGCTCGGCGCTCCACTCAGG	605
Db	547		606
		CCAGCTCGGCTACCAAGTGTGGGGCGCGGCTGTATCCAGCTCGGCGCTCCACTCAGG	
Qy	606	CCGGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGGAAACGGGCTTGA	665
Db	607		666
		CCGGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGGAAACGGGCTTGA	
Qy	666	ACCATAGCTCAGGAGCGCGGCTCCCTTGGGCTTGCCACGCCCGGGTGCAGGAGGC	725
Db	667		726
		ACCATAGCTCAGGAGCGCGGCTCCCTTGGGCTTGCCAGGCCCGGGTGCAGGAGGC	
Qy	726	CGGGGGCAGTGCCAGCCGAAGTCTGCCGTTTGCCCAAGAGGCCCGAGGCTGGCGTGCC	785

Db	1807	TGCAAGCATTTGGAAATAGACAGACACTTTGAAGAGGGTGCAGCTGCGGGAGCTGTGCGAAG	1866
QY	1866	CAGAGGTTCAGGCAGCATCGGAAGCCAGGCGCGCCTGCTGACGTCCAGACTCCGCTTCA	1925
Db	1867	CAGAGTTCAGGCAGCATCGGAAGCCAGGCGCGCCTGCTGACGTCCAGACTCCGCTTCA	1926
QY	1926	TCCCCAAGCCTGACGGGTGGGGCGATTGTGAACATGGACTGACTGCTGGGAGCCAGAA	1985
Db	1927	TCCCCAAGCCTGACGGGTGGGGCGATTGTGAACATGGACTGACTGCTGGGAGCCAGAA	1986
QY	1986	CGTTCCGACAGAAAGAGGCGGAGCTCTACCTCGAGGGTGAAGCACTGTTTCAGCG	2045
Db	1987	CGTTCCGACAGAAAGAGGCGGAGCTCTACCTCGAGGGTGAAGCACTGTTTCAGCG	2046
QY	2046	TGCTCAACTACAGCGGGCGGGCGCCCGGCTCCTGGGCGCTGTGCTGGGCGCTG	2105
Db	2047	TGCTCAACTACAGCGGGCGGGCGCCCGGCTCCTGGGCGCTGTGCTGGGCGCTG	2106
QY	2106	AGGATATCCACAGGGCCTGGGCGACCTTTCGTGCTCGGTGGGGGCCAGGACCGCGCG	2165
Db	2107	AGGATATCCACAGGGCCTGGGCGACCTTTCGTGCTCGGTGGGGGCCAGGACCGCGCG	2166
QY	2166	CTGAGCTGTACTTTCGAAGGTGGATGTACGGGCGCGTACCACACCATCCGCCAGGACA	2225
Db	2167	CTGAGCTGTACTTTCGAAGGTGGATGTACGGGCGCGTACCACACCATCCGCCAGGACA	2226
QY	2226	GGCTCACGGAGTCTATGCCAGCATCATCAAAACCCAGAACAGTACTGCTGCTCGGT	2285
Db	2227	GGCTCACGGAGTCTATGCCAGCATCATCAAAACCCAGAACAGTACTGCTGCTCGGT	2286
QY	2286	ATGCGGTGTCAGAAAGCGGCCATVGGGACAGTCCGACAGGCTTCAAGACCCAGTCT	2345
Db	2287	ATGCGGTGTCAGAAAGCGGCCATVGGGACAGTCCGCAAGGCTTCAAGAGCCACGTCT	2346
QY	2346	CTACCTTGACAGACCTTCAGCCGCTACATCGGACAGTTCGTGCTCACCTGCAGGAGACCA	2405
Db	2347	CTACCTTGACAGACCTTCAGCCGCTACATCGGACAGTTCGTGCTCACCTGCAGGAGACCA	2406
QY	2406	GCCCCGTGAGGATGCCGTGCTATCGAGCAGAGTCTCTCCCTGAATGAGGCCAGCAGTG	2465
Db	2407	GCCCCGTGAGGATGCCGTGCTATCGAGCAGAGTCTCTCCCTGAATGAGGCCAGCAGTG	2466
QY	2466	GCCTTTTGACGCTTCTTACGCTTCAATGTGCCACACGCCCTGGGCATCAGGGGCAAGT	2525
Db	2467	GCCTTTTGACGCTTCTTACGCTTCAATGTGCCACACGCCCTGGGCATCAGGGGCAAGT	2526
QY	2526	CCTAGCTTCAGTGCAGGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTCTGCAGCC	2585
Db	2527	CCTAGCTTCAGTGCAGGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTCTGCAGCC	2586
QY	2586	TGTGTACGGGACATGGAAACAAAGCTGTTTGGGGGATTCGGCGGGACGGGCTGCTCC	2645
Db	2587	TGTGTACGGGACATGGAAACAAAGCTGTTTGGGGGATTCGGCGGGACGGGCTGCTCC	2646
QY	2646	TGCGTTTGTGTGATTTCTTTGTTGGTGACACCTCACCTCACCCACCGGAAACCTTCC	2705
Db	2647	TGCGTTTGTGTGATTTCTTTGTTGGTGACACCTCACCTCACCCACCGGAAACCTTCC	2706
QY	2706	TCAGGACCTTGTCCGAGGTGCTCTGAGTATGGGTGCGTGGTGAACCTTGGGAAACAG	2765
Db	2707	TCAGGACCTTGTCCGAGGTGCTCTGAGTATGGGTGCGTGGTGAACCTTGGGAAACAG	2766
QY	2766	TGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAAGCGCTTTTGTTCAGATCCGG	2825
Db	2767	TGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAAGCGCTTTTGTTCAGATCCGG	2826
QY	2826	CCACGGCCTATTCGCCCTGGTGGGCTGCTGCTGGATACCGGACCCCTGGAGTGCAGA	2885
Db	2827	CCACGGCCTATTCGCCCTGGTGGGCTGCTGCTGGATACCGGACCCCTGGAGTGCAGA	2886
QY	2886	GGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCACCGGGGCT	2945
Db	2887	GGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCACCGGGGCT	2946
QY	2946	TCAAGGCTGGGAGAACATGCGTCCAAACCTCTTTGGGCTCTTGGGCTGAAGTGTCA	3005
Db	2947	TCAAGGCTGGGAGAACATGCGTCCAAACCTCTTTGGGCTCTTGGGCTGAAGTGTCA	3006
QY	3006	GCCTGTTTCTGTGATTTGAGGTGAACAGCTCCAGAGGTGTGCACCAACATCTACAAGA	3065
Db	3007	GCCTGTTTCTGTGATTTGAGGTGAACAGCTCCAGAGGTGTGCACCAACATCTACAAGA	3066
QY	3066	TCCTCTGCTGAGCGGTACAGGTTTTCAGCATGTGTGCTGAGCTCCCATTTTCATCAG	3125
Db	3067	TCCTCTGCTGAGCGGTACAGGTTTTCAGCATGTGTGCTGAGCTCCCATTTTCATCAG	3126
QY	3126	AAGTTTGGAAACCCACATTTTCTGCGGCTCATCTCTGACAGGCTCCCTCTGCT	3185
Db	3127	AAGTTTGGAAACCCACATTTTCTGCGGCTCATCTCTGACAGGCTCCCTCTGCT	3186
QY	3186	ACTCCATCTCTGAAAGCCAAAGCAGGATGTGCTGGGGGCCAAGGGCGCGCGGCC	3245
Db	3187	ACTCCATCTCTGAAAGCCAAAGCAGGATGTGCTGGGGGCCAAGGGCGCGCGGCC	3246
QY	3246	CTCTGCCCTCCGAGGCGGTGCAAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCTGACT	3305
Db	3247	CTCTGCCCTCCGAGGCGGTGCAAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCTGACT	3306
QY	3306	GACACGCTGTACCTTACGTGCCACTCTCTGGGTCTACTCAGGACAGCCAGCAGCTGA	3365
Db	3307	GACACGCTGTACCTTACGTGCCACTCTCTGGGTCTACTCAGGACAGCCAGCAGCTGA	3366
QY	3366	GTCCGNAAGTCCCGGGGAGAGCTGACTGCCCTGGAGGCCGAGCCACCCGGGCTGC	3425
Db	3367	GTCCGNAAGTCCCGGGGAGAGCTGACTGCCCTGGAGGCCGAGCCACCCGGGCTGC	3426
QY	3426	CCTCAGACTTCAAGACCATCTCTGGACTGATGCCACCCACAGCCAGGCGGAGAGCA	3485
Db	3427	CCTCAGACTTCAAGACCATCTCTGGACTGATGCCACCCACAGCCAGGCGGAGAGCA	3486
QY	3486	GACACAGAGCCCTGTACGCGGGCTCTACTCTCCAGGAGGGAGGGCGGCCACAC	3545
Db	3487	GACACAGAGCCCTGTACGCGGGCTCTACTCTCCAGGAGGGAGGGCGGCCACAC	3546
QY	3546	CCAGGCCCGCAGCGCTGGGAGTCTGAGGCTTGAAGTGTGTTGGCGGAGGCTGATGT	3605
Db	3547	CCAGGCCCGCAGCGCTGGGAGTCTGAGGCTTGAAGTGTGTTGGCGGAGGCTGATGT	3606
QY	3606	CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGTGTGAGTGTGTTGGCGGAGGCTGATGT	3665
Db	3607	CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGTGTGAGTGTGTTGGCGGAGGCTGATGT	3666
QY	3666	TCAGACACCTGCGCTTTCATTTCCCAAGGCTGGGCTGCGGCTCCACCCAGGGCC	3725
Db	3667	TCAGACACCTGCGCTTTCATTTCCCAAGGCTGGGCTGCGGCTCCACCCAGGGCC	3726
QY	3726	AGCTTTTCTTCCACAGGCGCGGCTTCCACTCCCAATAGGAATAGTCCATCCCCAGA	3785
Db	3727	AGCTTTTCTTCCACAGGCGCGGCTTCCACTCCCAATAGGAATAGTCCATCCCCAGA	3786
QY	3786	TTCCGCTTGTTCACCCCTGCGCTTCCCTTTCCTTTCCACCCCGCCACCATCCAGGTG	3845
Db	3787	TTCCGCTTGTTCACCCCTGCGCTTCCCTTTCCTTTCCACCCCGCCACCATCCAGGTG	3846
QY	3846	GAGACCTTGAGAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTG	3905
Db	3847	GAGACCTTGAGAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTG	3906
QY	3906	TACACAGGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAATTTGGGGGAGGT	3965
Db	3907	TACACAGGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAATTTGGGGGAGGT	3966
QY	3966	GCTGTGGGAGTAAATACATATATAGTGTGTTTTCAGTTTCAAAAAA 4015	
Db	3967	GCTGTGGGAGTAAATACATATATAGTGTGTTTTCAGTTTCAAAAAA 4016	

Dd	967	ACGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGCCCTTGTCGCCGG	1026
QY	1026	TGTACGCCGAGACAAAGCACTTCCCTACTCTCCTACGCGACAAAGGAGCAGCTGCGCCCT	1085
Dd	1027	TGTACGCCGAGACAAAGCACTTCCCTACTCTCCTACGCGACAAAGGAGCAGCTGCGCCCT	1086
QY	1086	CGTTCCTACTCAGCTCTCTGAGGCCAGCCTGACTGCTGGCCTCGGAGGCTCGTGAGACCA	1145
Dd	1087	CGTTCCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCCTCGGAGGCTCGTGAGACCA	1146
QY	1146	TCCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCGCTGCCCC	1205
Dd	1147	TCCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCGCTGCCCC	1206
QY	1206	AGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAAGCGCAGTGCC	1265
Dd	1207	AGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAAGCGCAGTGCC	1266
QY	1266	CCTACGGGTGCTCCTCAAGACGCACTGCCCGTGCAGCTGGGTCAGCGGTCACCCAGCAGCG	1325
Dd	1267	CCTACGGGTGCTCCTCAAGACGCACTGCCCGTGCAGCTGGGTCAGCGGTCACCCAGCAGCG	1326
QY	1326	GTGTCTGTGCCGGGAAGCCCAAGGCTCTGTGCGGCCCCCGAGGAGGAGACACAG	1385
Dd	1327	GTGTCTGTGCCGGGAAGCCCAAGGCTCTGTGCGGCCCCCGAGGAGGAGACACAG	1386
QY	1386	ACCCCGTGCCTGTGTGAGCTGTCTCCGCCAGACAGACCCCTGGCAGGTGTACGGCT	1445
Dd	1387	ACCCCGTGCCTGTGTGAGCTGTCTCCGCCAGACAGACCCCTGGCAGGTGTACGGCT	1446
QY	1446	TGCTGCGGCCCTGCCCTGCGGCCGCTGCTGCGGCCCGCCAGGCTCTGGGCTCCAGGCACAG	1505
Dd	1447	TGCTGCGGCCCTGCCCTGCGGCCGCTGCTGCGGCCCGCCAGGCTCTGGGCTCCAGGCACAG	1506
QY	1506	AAGCGCGCTTCCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT	1565
Dd	1507	AAGCGCGCTTCCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT	1566
QY	1566	CGCTCAGAGCTGAGCTGGAAGATGAGCTGCGGAGCTGCGCTTGGCTGCGCAGAGCC	1625
Dd	1567	CGCTCAGAGCTGAGCTGGAAGATGAGCTGCGGAGCTGCGCTTGGCTGCGCAGAGCC	1626
QY	1626	CAGGGTGTGCTGTGTCGGCGCAGACCGCTCTGCTGAGGAGATCCCTGGCCCAAGT	1685
Dd	1627	CAGGGTGTGCTGTGTCGGCGCAGACCGCTCTGCTGAGGAGATCCCTGGCCCAAGT	1686
QY	1686	TCTGCACTGGCTGATGAGTGTACGTCTGCTGAGCTGCTCAGCTCTTTCTTTATGTCA	1745
Dd	1687	TCTGCACTGGCTGATGAGTGTACGTCTGCTGAGCTGCTCAGCTCTTTCTTTATGTCA	1746
QY	1746	CGGAGACAGCTTCAAAAAGACAGCTCTTTTCTACCGGAAGAGTGCTGGAGCAAGT	1805
Dd	1747	CGGAGACAGCTTCAAAAAGACAGCTCTTTTCTACCGGAAGAGTGCTGGAGCAAGT	1806
QY	1806	TGCAAAAGCATTGAATCAGACAGCACTTGAAGAGGTGACGTGCGGGAGCTCTCGGAAG	1865
Dd	1807	TGCAAAAGCATTGAATCAGACAGCACTTGAAGAGGTGACGTGCGGGAGCTCTCGGAAG	1866
QY	1866	CAGAGTCAAGCAGCATCGGGAAGCAGCGCCGCTGCTGAGCTCCAGACTCCGCTTCA	1925
Dd	1867	CAGAGTCAAGCAGCATCGGGAAGCAGCGCCGCTGCTGAGCTCCAGACTCCGCTTCA	1926
QY	1926	TCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGACATGACACTGCTGCGGAGCCAGAA	1985
Dd	1927	TCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTACGTCGTGGGAGCCAGAA	1986
QY	1986	CGTTCCGACAGAAAAAGGGCGGAGCTCTACCTCGAGGGTGAAGGCACTGTTACAGC	2045
Dd	1987	CGTTCCGACAGAAAAAGGGCGGAGCTCTACCTCGAGGGTGAAGGCACTGTTACAGC	2046
QY	2046	TGCTCAACTACGAGCGGGCGCGGCCCTCCTGGCGGCTCTGTGCTGGGCTGG	2105
Dd	2047	TGCTCAACTACGAGCGGGCGCGGCCCTCCTGGCGGCTCTGTGCTGGGCTGG	2106
QY	2106	ACGATATCCACAGGGCTTGGCGCACCTTCTGCTGCTGTGTCGCGGCCACAGACCCCGCGC	2165
Dd	2107	ACGATATCCACAGGGCTTGGCGCACCTTCTGCTGCTGTGTCGCGGCCACAGACCCCGCGC	2166
QY	2166	CTGAGCTGTACTTTTGTCAAGGTGGATGTGAGGGCGGCTGACAGACCATCCTCCCGAGACA	2225
Dd	2167	CTGAGCTGTACTTTTGTCAAGGTGGATGTGAGGGCGGCTGACAGACCATCCTCCCGAGACA	2226
QY	2226	GGCTCAGGAGGTCAATCGCCAGCATCAAAACCCAGAACACGTACTGCTGCTGGGT	2285
Dd	2227	GGCTCAGGAGGTCAATCGCCAGCATCAAAACCCAGAACACGTACTGCTGCTGGGT	2286
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Dd	2287	ATGCCGTGTCCAGAAAGCGGCCCATGGGCACATGCCCAAGGCTTTCAAGAGCCACGTCT	2346
QY	2346	CTACCTTGACAGACCTTCCAGCCCTACATGCGACAGTTCGTGGCTCAGCTCAGAGACCA	2405
Dd	2347	CTACCTTGACAGACCTTCCAGCCCTACATGCGACAGTTCGTGGCTCAGCTCAGAGACCA	2406
QY	2406	GCCCGTGTAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCCTGAATGAGCCAGCAGTG	2465
Dd	2407	GCCCGTGTAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCCTGAATGAGCCAGCAGTG	2466
QY	2466	GCCTCTTGACAGCTTCTCTACGTTTATGTGCCACACGCCGTGCCGATCAGGGGCAAGT	2525
Dd	2467	GCCTCTTGACAGCTTCTCTACGTTTATGTGCCACACGCCGTGCCGATCAGGGGCAAGT	2526
QY	2526	CCTACCTTGACAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTGAGCC	2585
Dd	2527	CCTACCTTGACAGTCCCGAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTGAGCC	2586
QY	2586	TGTGCTACGCGACATGGAGAACAAAGCTGTTGCGGGATTCGCGGGAGCGGCTGCTCC	2645
Dd	2587	TGTGCTACGCGACATGGAGAACAAAGCTGTTGCGGGATTCGCGGGAGCGGCTGCTCC	2646
QY	2646	TGCGTTTGTGGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCGAANAACCTTCC	2705
Dd	2647	TGCGTTTGTGGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCGAANAACCTTCC	2706
QY	2706	TCAGGACCTTGTCGCGAGGTGCTCCCTGAGTATGGCTGCGTGGTGAACCTTTCGGAAGACAG	2765
Dd	2707	TCAGGACCTTGTCGCGAGGTGCTCCCTGAGTATGGCTGCGTGGTGAACCTTTCGGAAGACAG	2766
QY	2766	TGCTGAACCTTCCCTGTAGAAAGACAGGCCCTGGGTGCGACGCTTTTGTTCAGATGCCGG	2825
Dd	2767	TGCTGAACCTTCCCTGTAGAAAGACAGGCCCTGGGTGCGACGCTTTTGTTCAGATGCCGG	2826
QY	2826	CCACAGCCCTATTCCCTGTGGTGGGCTGCTGCTGGATACCCGAGCCCTGGAGGTGCAGA	2885
Dd	2827	CCACAGCCCTATTCCCTGTGGTGGGCTGCTGCTGGATACCCGAGCCCTGGAGGTGCAGA	2886
QY	2886	GCAGCTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGGGCT	2945
Dd	2887	GCAGCTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGGGCT	2946
QY	2946	TCAAGGCTGGGAGAAACATGCTGCGAAACTCTTTGGGGTCTTTGCGGCTGAAGTGTACCA	3005
Dd	2947	TCAAGGCTGGGAGAAACATGCTGCGAAACTCTTTGGGGTCTTTGCGGCTGAAGTGTACCA	3006
QY	3006	GCCTGTTTCTGGATTTCAGAGTGAACAGCCCTCAGAGGCTGTCACCAACATCTACAGA	3065
Dd	3007	GCCTGTTTCTGGATTTCAGAGTGAACAGCCCTCCAGAGCGGTGTCACCAACATCTACAGA	3066
QY	3066	TCCTCTGCTGCGAGGCTACAGGTTTCACGATGTGTGCTGACAGCTCCCATTTTCATCAGC	3125
Dd	3067	TCCTCTGCTGCGAGGCTACAGGTTTCACGATGTGTGCTGACAGCTCCCATTTTCATCAGC	3126
QY	3126	AAGTTTGGAGAAACCCACATTTTCTGCGCGCTCATCTCTGACAGGCTCCCTCTGCT	3185
Dd	3127	AAGTTTGGAGAAACCCACATTTTCTGCGCGCTCATCTCTGACAGGCTCCCTCTGCT	3186

QY	3186	ACTCCATCCTGAAGCCNAGAACGACGAGGATGTGGCTGGGGGCCAAGGGGCGCCGCGGCC	3245
Db	3187	ACTCCATCCTGAAGCCNAGAACGAGGATGTGGCTGGGGGCCAAGGGGCGCCGCGGCC	3246
QY	3246	CTCTGCCCTCCGAGGCGGTGAGTGGCTGCCACCAAGCATTCCTGCTCAAGCTGACTC	3305
Db	3247	CTCTGCCCTCCGAGGCGGTGAGTGGCTGCCACCAAGCATTCCTGCTCAAGCTGACTC	3306
QY	3306	GACACCGGTGTCACCTAGCTGCCACTCCTTGGGGTCACTCAGGACAGCCAGACGCGAGCTGA	3365
Db	3307	GACACCGGTGTCACCTAGCTGCCACTCCTTGGGGTCACTCAGGACAGCCAGACGCGAGCTGA	3366
QY	3366	GTCGGAAGTCCCGGGGACGAGCTGACTGCCCTGGAGGCGCAGCCAAACCCGGGACTGC	3425
Db	3367	GTCGGAAGTCCCGGGGACGAGCTGACTGCCCTGGAGGCGCAGCCAAACCCGGGACTGC	3426
QY	3426	CCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCCAGCCAGCCAGGCGCGAGCA	3485
Db	3427	CCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCCAGCCAGGCGCGAGGCA	3486
QY	3486	GACACCAAGCCCTGTACGCCGGGCTTACGTCCCAGGAGGGGCGGGCCACAC	3545
Db	3487	GACACCAAGCCCTGTACGCCGGGCTTACGTCCCAGGAGGGGCGGGCCACAC	3546
QY	3546	CCAGGCGCGCACCGCTGGGAGTCTCAGGCCCTGAGTGTGTTGGCCGAGGCCCTGCATGT	3605
Db	3547	CCAGGCGCGCACCGCTGGGAGTCTCAGGCCCTGAGTGTGTTGGCCGAGGCCCTGCATGT	3606
QY	3606	CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGGGCTGAGTG	3665
Db	3607	CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGGGCTGAGTG	3666
QY	3666	TCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCCAGCCACCCAGGGCC	3725
Db	3667	TCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCCAGCCACCCAGGGCC	3726
QY	3726	AGCTTTTCTCACCAGGAGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCCCAGA	3785
Db	3727	AGCTTTTCTCACCAGGAGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCCCAGA	3786
QY	3786	TTCCGCAATGTTACCCCTCGCCCTGCGCTCCTTTGCTTCCACCCACCATCCAGGTG	3845
Db	3787	TTCCGCAATGTTACCCCTCGCCCTGCGCTCCTTTGCTTCCACCCACCATCCAGGTG	3846
QY	3846	GAGACCCGTGAAGAGACCTCGGAGCTCTGGAAATTTGGAGTGACCAAAAGGTGTGCCCTG	3905
Db	3847	GAGACCCGTGAAGAGACCTCGGAGCTCTGGAAATTTGGAGTGACCAAAAGGTGTGCCCTG	3906
QY	3906	TACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATGGGGGGAGGT	3965
Db	3907	TACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATGGGGGGAGGT	3966
QY	3966	GCTGTGGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTTGAAAAAA 4015	
Db	3967	GCTGTGGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTTGAAAAAA 4016	

Search completed: October 14, 2003, 22:27:52
Job time : 1008 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 22:11:08 ; Search time 219 Seconds
(without alignments)
8092.024 Million cell updates/sec

Title: US-10-054-295-224

Perfect score: 4015

Sequence: 1 GCAGCGCTGCGCTGCTGC.....TTTTTCAGTTTGAAGAAA 4015

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/2/lna/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/lna/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/lna/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/lna/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/lna/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4015	100.0	4015	3	US-08-851-843A-224 ✓
2	4015	100.0	4015	3	US-08-974-549A-1 ✓
3	4015	100.0	4015	3	US-08-854-050-224 ✓
4	4015	100.0	4015	4	US-09-430-323-224 ✓
5	4015	100.0	4015	4	US-09-572-423B-3 ✓
6	4015	100.0	4015	4	US-09-128-354-1 ✓
7	4015	100.0	4015	4	US-09-675-321-1 ✓
8	4015	100.0	4015	4	US-09-052-919-1 ✓
9	4015	100.0	4015	4	US-08-912-951-1 ✓
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11	4008.6	99.8	4037	3	US-08-974-549A-343
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15	3849.2	95.9	4029	4	US-09-430-323-173
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ALIGNMENTS

RESULT 1
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; Sequence 224, Application US/08051843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/846,017
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/844,419
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/724,643
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00293005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:

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RESULT 2

US-08-974-549A-1

; Sequence 1, Application US/08974549A

; Patent No. 6166178

NW

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610DS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56...3454

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component"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	3481	GAGCAGACCAAGCAGCCGTGTACGCCGGGCTTACGTCCTCAGGAGGAGGAGGGCGGCC	3540
Db	3481	GAGCAGACCAAGCAGCCGTGTACGCCGGGCTTACGTCCTCAGGAGGAGGAGGGCGGCC	3540
QY	3541	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAAGTGTGTCGCCAGGCGCTG	3600
Db	3541	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAAGTGTGTCGCCAGGCGCTG	3600
QY	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGACGAGTGTCCAGCCAAAGGCT	3660
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Db	121	GCCTGTGGCACGTTCTGCGGCGCCCTGGGGCCCCAGGGCTGGCGGCTGTGTGCACCGCGG	180
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2

;; FILLING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 224:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4015 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 56..3454
;; OTHER INFORMATION: /product= "hprt"
;; /note= "human telomerase reverse
;; transcriptase (hTERT) catalytic protein
;; component"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-430-323-224

Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCGCGTCCCGGTGCGGAGCGGTGCGCTCCCTGCTGGCAGGCACCTACGCGAGGTGCT 120
QY 121 GCGCGTGGCAGCTTTCGCGCGCTGCTGGGCGCCAGAGGCTGCGCTGGTGGAGCGCG 180
DB 121 GCGCGTGGCAGCTTTCGCGCGCTGCTGGGCGCCAGAGGCTGCGCTGGTGGAGCGCG 180
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DB 181 GGACCGGGGGCTTTCGCGCGCTGCTGGCAGCTGCTGGTGGTGGTGGTGGAGCGC 240
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DB 241 ACGGCGCGCGCGCGCGCGCTGCTGGCAGAGTGTGCTGGTGGAGAGCTGGTGGC 300
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DB 421 CTTGCCCAACACAGGTGACCGACCTGCGGGGGAGCGGGGGCGGGGGCGGGGGCGGG 480
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DB 961 GCACGAGCGGGCG 1020
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QY 1141 GACCATCTTCTGGGTTCAGGCGCTGGATGCCAGGACTCCCGCGAGGTGCGCGCGCT 1200
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QY 1441 CGGCTTGTGCGGGGCTGCTGCGCGGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
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DB 1561 GCTCTCGCTCAGGAGCTGAGCTGGAAGATGAGGCTGCGGACTGCGCTTGGTGGCGAG 1620
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Db 2821 GCCGCCACAGCCCTATTTCCCTGTGTGGCGCTGTGTGGATACCCGACCCCTGGAGT 2880
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RESULT 7

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; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR FILING DATE: 1998-03-31
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-09-675-321-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2221	GGACAGGCTCACGGAGGTCTATCGCCACGATCATCAAAACCCAGAAACACGTACTGCGTGGC	2280
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Db	2281		
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QY	2341	CGTCTCTACCTTGACACAGCCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTCTGAGGA	2400
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QY	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
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QY	3061	CAAGATCCTCCTGCTGACGGCGTACAGTTTCACGCATGTGTGTCGAGCTCCCATTTCA	3120
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QY	3121	TCAGCAAGTTTGGAAACCCACATTTTTCCTGGGGTCACTCTGACACGGCCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAAACCCACATTTTTCCTGGGGTCACTCTGACACGGCCTCCCT	3180
QY	3181	CTGCTACTCCATCCTGAAAGCCAGACGAGGATGTCGCTGGGGCCCAAGGCCGCC	3240
Db	3181	CTGCTACTCCATCCTGAAAGCCAGACGAGGATGTCGCTGGGGCCCAAGGCCGCC	3240
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Db	3241	CGGCCCTCTGCCCTCCAGGCCGTGCTAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
QY	3301	GACTCGACACCGTGTACCTACGTGGCACTCCTGGGGTCACTCAGACAGCCAGACGCA	3360
Db	3301	GACTCGACACCGTGTACCTACGTGGCACTCCTGGGGTCACTCAGACAGCCAGACGCA	3360

QY 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTCCCTTGAGGCGGACGCAACCCCGGC 3420
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DB 3481 GAGCAGACACCAAGCAGCCTGTACGCGGGGCTTACGTCCAGGAGGAGGGGCGGCC 3540
QY 3541 CACACCCAGGCGGCGGAGTCTGAGGCTTGTAGGCTTGTAGTGTGGCGGAGGCGCTG 3600
DB 3541 CACACCCAGGCGGCGGAGTCTGAGGCTTGTAGGCTTGTAGTGTGGCGGAGGCGCTG 3600
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DB 3601 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGGCT 3660
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QY 3781 CCAGATTGCCATTTCTTACCCCTCGCCCTGCGCTTCTGCTTCCACCCCGCCACATCC 3840
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RESULT 8
US-09-052-919-1
Sequence 1, Application US/09052919
Patent No. 6444650
GENERAL INFORMATION: V
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-0036000US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (hTRT)"
US-09-052-919-1

Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGGACGCTACCGCGAGGTGCT 120

QY	121	GC	CGTGGCCACAGTTCTGTCGGCGCGCTGGGGCCCCAAGGGCTGGCGGCTGGTGTCACGCGG	180
DB	121	GC	CGTGGCCACGTTCTGTGCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGTCACGCGG	180
QY	181	GG	ACCGCGCGCTTTCGCGCGCTGTGGGCCACGTGCTGTGTGCTGTGCGCTGGGACGC	240
DB	181	GG	ACCGCGCGCTTTCGCGCGCTGTGGGGCCAGTGTGCTGTGTGCTGTGCGCTGGGACGC	240
QY	241	AC	GGCGCGCCCCCGCGCGCCCTCTTCCGCGAGGTGCTCTGAAGAGCTGGTGGC	300
DB	241	AC	GGCGCGCCCCCGCGCGCCCTCTTCCGCGAGGTGCTCTGAAGAGCTGGTGGC	300
QY	301	CC	GAGTGTGCAGAGGCTGTGCGAGCGGGCGCGAAGACGTGCTGGCTTCGCTTCGCCTTCGC	360
DB	301	CC	GAGTGTGCAGAGGCTGTGCGAGCGGGCGCGAAGACGTGCTGGCTTCGCTTCGCTTCGC	360
QY	361	GT	CTGTGACGGGGCGCGCGGGGCCCTTCCGCGAGGCTTACACACGCTGCGCAGCTA	420
DB	361	GT	CTGTGTGACGGGGCGCGGGGGCCCCCGAGGCTTACACACGCTGCGCAGCTA	420
QY	421	CT	GCCCCAACAGGTGACCGACGACATGCGGGGAGCGGGGCTGGGGCTGCTGCTGCG	480
DB	421	CT	GCCCCAACAGGTGACCGACGACATGCGGGGAGCGGGGCTGGGGCTGCTGCTGCG	480
QY	481	CC	GGTGGGCGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540
DB	481	CC	GGTGGGCGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540
QY	541	GG	CTCCAGCTGCGCTACCAAGTGTGCGGGCGCGCGCTGTACAGCTCGGCGCTGCGC	600
DB	541	GG	CTCCAGCTGCGCTACCAAGTGTGCGGGCGCGCGCTGTACAGCTCGGCGCTGCGC	600
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DB	661	CT	GAAACATAGCTCAGGAGGCGCGGGTCCCTGGGCTGCCAGCGCGCGGCTGGGAG	720
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DB	721	GAG	CGGGGCGAGTGCACGCAAGCTGCGGCTGGCGCTGCCAAGAGGCCAGGCGTGGCG	780
QY	781	TG	CCCCTGAGCGGAGCGGACGCGCGTGGCGAGGGTCTCTGGGCCACACCGGGCAGGAC	840
DB	781	TG	CCCCTGAGCGGAGCGGACGCGCGTGGCGAGGGTCTCTGGGCCACACCGGGCAGGAC	840
QY	841	CG	TGGACCGAGTACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
DB	841	CG	TGGACCGAGTACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
QY	901	CA	CTCTTTGGAGGGTGGCTCTGTGCGACGCGCCACTCCGACCTCCGTTGGGCGCGCA	960
DB	901	CA	CTCTTTGGAGGGTGGCTCTGTGCGACGCGCCACTCCGACCTCCGTTGGGCGCGCA	960
QY	961	GC	ACCGCGGGCCCCCATCCATCGCGGCCACACGCTCCCTGGGACAGCGCTTCG	1020
DB	961	GC	ACCGCGGGCCCCCATCCATCGCGGCCACACGCTCCCTGGGACAGCGCTTCG	1020
QY	1021	CC	CGGTGTACCGGAGACCAAGCACTTCTTCTACTCTCTCTCTCTCTCTCTCTCTCTCT	1080
DB	1021	CC	CGGTGTACCGGAGACCAAGCACTTCTTCTACTCTCTCTCTCTCTCTCTCTCTCTCT	1080
QY	1081	GC	CTCTTCTACTAGCTCTCTGAGGGCCAGCCTGACTGTGGGCTCGGAGGCTCTGTTGA	1140
DB	1081	GC	CTCTTCTACTAGCTCTCTGAGGGCCAGCCTGACTGTGGGCTCGGAGGCTCTGTTGA	1140
QY	1141	GA	CCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT	1200
DB	1141	GA	CCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT	1200
QY	1201	GC	CCCCACGCTACTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACACACGCGCA	1260

Db	1201	 GCCCCAGGCTACTGGCAAAATGCGGCCCTCTGTTTCTGGAGCTGTTGGGAACACACGCGCA	1260	
QY	1261	 GTGCCCTACGGGTGCTCTCTAAGACGCACACTGCCCCGCTCGGAGCTCGGCTACCCGACG	1320	
Db	1261	 GTGCCCTACGGGTGCTCTCTAAGACGCACACTGCCCGCTCGGAGCTCGGCTACCCGACG	1320	
QY	1321	 AGCCGGTGTCTGTGCTCCCGGAGAAAGCCCCAGGGTCTGTGGCGGCCCGCGAGAGAGGA	1380	
Db	1321	 AGCCGGTGTCTGTGCTCCCGGAGAAAGCCCCAGGGCTGTGTGGCGGCCCGCGAGAGAGGA	1380	
QY	1381	 CACAGACCCCGTCGCCCTGTGTGACGTGCTCCGCGACACAGCAGCCCTTGGCAGGTGA	1440	
Db	1381	 CACAGACCCCGTCGCCCTGTGTGACGTGCTCCGCGACACAGCAGCCCTTGGCAGGTGA	1440	
QY	1441	 CGGCTTCGTGGGGGCTTCCTCGGCCCGGCTGGTGCCCCAGGCTCTGGGGCTCCAGGCA	1500	
Db	1441	 CGGCTTCGTGGGGGCTTCCTCGGCCCGGCTGGTGCCCCAGGCTCTGGGGCTCCAGGCA	1500	
QY	1501	 CAACGAACCGGCTTCCTCAGGAACACCAAGAAGTTCACTCCCTGGGAGCATGCCAA	1560	
Db	1501	 CAACGAACCGGCTTCCTCAGGAACACCAAGAAGTTCACTCCCTGGGAGCATGCCAA	1560	
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Db	1561	 GCTCTCGCTCAGAGAGTGACGTGGAAAGATGACGGCTGCGGAGCTGGCTGGCTGCGCAG	1620	
QY	1621	 GAGCCCCAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTCGCTGAGAGATCCTGGC	1680	
Db	1621	 GAGCCCCAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTCGCTGAGAGATCCTGGC	1680	
QY	1681	 CAAGTTCCTGCACTCGGCTGATGAGTGTACGTCTGTCGAGCTGCTCAGGTCTTCTTTTA	1740	
Db	1681	 CAAGTTCCTGCACTCGGCTGATGAGTGTACGTCTGTCGAGCTGCTCAGGTCTTCTTTTA	1740	
QY	1741	 TGTCACGGAGACACGTTTCAAAGAACACAGGCTCTTTTCTACCGAAGAGTGTCTGAG	1800	
Db	1741	 TGTCACGGAGACACGTTTCAAAGAACACAGGCTCTTTTCTACCGAAGAGTGTCTGAG	1800	
QY	1801	 CAAGTTCGAAGCAATTGGAATCAGACAGCACTTGAAGAGGCTGACGCTGGGAGCTGTC	1860	
Db	1801	 CAAGTTCGAAGCAATTGGAATCAGACAGCACTTGAAGAGGCTGACGCTGGGAGCTGTC	1860	
QY	1861	 GGAAGCAGAGGTTCAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACCTCCAGACTCG	1920	
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QY	1921	 CTTTCATCCCAAGCCTGACGGCTGCGGCCGATTTGTAACATGAGTACGTGCTGGGAGC	1980	
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Db	1981	 CAGAACCTTCCGACAGAAAAGGGCCGAGCCTCTCACCTCGAGGCTGAAGSCACTGT	2040	
QY	2041	 CAGCGTCTCAACTACAGCGGGGCGGGCCCGCCGCTCTCTGGGCGCTCTGTGCTGG	2100	
Db	2041	 CAGCGTCTCAACTACAGCGGGGCGGGCCCGCCGCTCTCTGGGCGCTCTGTGCTGG	2100	
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QY	2221	 GGACAGCTCAGCGAGGTCTATCCGACGATCATCAAAACCCAGAACACGTACTGGCTGG	2280	
Db	2221	 GGACAGCTCAGCGAGGTCTATCCGACGATCATCAAAACCCAGAACACGTACTGGCTGG	2280	
QY	2281	 TCGGTATTCGGTGGTCCAGAAAGCCGCCATGGCACGTCCGCAAGGCCCTTCAAGAGCCA	2340	

2281	Db	TCGGTATGCGGTGCTCCAGAAAGCGCGCCCAATGGGCGACGTCCCGCAAGGCCCTTCAAGAGCCA	2341
2341	QY	CGTCTCTACCTTGACACAGACCTCCAGCCGTACATGCGACAGATTGCTGGCTCACCTGCAGGA	2400
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2641	Db	GCCTCCGCTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAC	2700
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2821	Db	GCGGGCCCCAGGCGCTATTCCCGTGGTGGCGGCTGCTGCTGGATACCCGGACCCCTGAGGT	2880
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RESULT 9

US-08-912-951-1

US-08-912-931-I
: Sequence 1: Application US/08912951

Sequence 1, Applicant
Patent No. 6475789

: FACILE NO: 0473789
: GENERAL INFORMATION:

GENERAL INFORMATION: Cech, Thomas R.

APPLICANT: Linnar, Joachim

APPLICANT: LINGNER, JOACHIM
APPLICANT: NAKAMURA, TORII

APPLICANT: NAKAMURA, TORU
APPLICANT: Chapman, Karen B

APPLICANT: Chapman, Karen B

APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin

APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H

APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT.

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TITLE OF INVENTION:	HUMAN TELOMERASE CA

	TITLE OF INVENTION:	THIRD
	NUMBER OF SEQUENCES:	225

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; NUMBER OF SEQUENCES: 3
CORRESPONDENCE 'DEFEA

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; CORRESPONDENCE ADDRESS:

; ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarca

CITY: San Francisco

; STATE: California

; COUNTRY: U

; ZIP: 94111

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Rel

; CURRENT APPLICATION DATA:

COMMENT IN DETENTION DATA:
; APPLICATION NUMBER: US/08/912,951

APPLICATION NUMBER: 14-AUG-2014
FILING DATE: 14-AUG-2014

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; PRIOR APPLICATION DATA: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
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; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
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; TOPOLOGY: linear
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; OTHER INFORMATION: /product= "hprt"
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; OTHER INFORMATION: transcriptase (hprt) catalytic protein
; OTHER INFORMATION: component"
; US-08-912-951-1

Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCGCTGCTGCTGCGCACGTGGGAGCCCTGGCCCGGCCACCCCGCGATGCC 60
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Db 361 GCTGCTGGAGCGGCGCGCGGCGCGCCCGCGAGGCTTACCAACAGCGTGCAGCTA 420
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Qy 961 GCACCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Db 961 GCACCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Qy 1021 CCCGGTGTAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
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Qy 1081 GCGCTCTCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 1140
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Qy 1201 GCGCGCGCGCTACTGCGAAGTGGCGCGCTGTTCTGAGAGCTGCTGGGAAACACGCGCA 1260
Db 1201 GCGCGCGCGCTACTGCGAAGTGGCGCGCTGTTCTGAGAGCTGCTGGGAAACACGCGCA 1260
Qy 1261 GTGCGCGCTACGGGCTGCTCTCAAGCGCTGCGCGCTGCGAGCTGCGGTACCGCGCG 1320
Db 1261 GTGCGCGCTACGGGCTGCTCTCAAGCGCTGCGCGCTGCGAGCTGCGGTACCGCGCG 1320
Qy 1321 AGCGGCTGTGTCGCCGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Db 1321 AGCGGCTGTGTCGCCGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Qy 1381 CACAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 1381 CACAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Qy 1441 CGGCTTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
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QY	1501	CAACGAACGCCGCTTCCCTCAGGAACACCAAGAAAGTTCACTCCTCGGGGAAGCATGCCAA	1560	2581	CAGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
Db	1501	CAACGAACGCCGCTTCCCTCAGGAACACCAAGAAAGTTCACTCCTCGGGGAAGCATGCCAA	1560	2581	CAGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCT	2640
QY	1561	GCCTCTCGCTGCAGAGCTGACGTGGAAGATGACGCTGCGGACTCGCTTGGCTGGCGCAG	1620	2641	GCTCCTGCGCTTGGTGGATGATTTCTTGTGTGGTGACACCTCACTCACCACCGGAAAC	2700
Db	1561	GCCTCTCGCTGCAGAGCTGACGTGGAAGATGACGCTGCGGACTCGCTTGGCTGGCGCAG	1620	2641	GCTCCTGCGCTTGGTGGATGATTTCTTGTGTGGTGACACCTCACTCACCACCGGAAAC	2700
QY	1621	GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGCTCTCGTGAGGAGATCCTGGC	1680	2701	CTTCTCTCAGSACCCCTGGTCGAGGTGTCCTTGAGTATGGCTGGCTGTGTGAACCTTGGCGAA	2760
Db	1621	GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGCTCTCGTGAGGAGATCCTGGC	1680	2701	CTTCTCTCAGSACCCCTGGTCGAGGTGTCCTTGAGTATGGCTGGCTGTGTGAACCTTGGCGAA	2760
QY	1681	CAAGTTCCCTGCACTGCTGATGAGTGTACGTCTCGAGCTGCTCAGGTCTTTCTTTTA	1740	2761	GACAGTGTGTAACCTTCCCTGTAGAACAGAGGCCCTGGGTGCGACGCTTTTGTTCAGAT	2820
Db	1681	CAAGTTCCCTGCACTGCTGATGAGTGTACGTCTCGAGCTGCTCAGGTCTTTCTTTTA	1740	2761	GACAGTGTGTAACCTTCCCTGTAGAACAGAGGCCCTGGGTGCGACGCTTTTGTTCAGAT	2820
QY	1741	TGTCACGGAGACCACTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800	2821	GCCGGCCACAGGCTTATCCCTGTGGTGGCGCTGCTGGATACCGGACCTTGGAGGT	2880
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QY	1861	GGAAGCAGAGGTCAGGACGATCGGAAGCCAGCGCCGCTGCTGACGTCCAGACTCCG	1920	2941	CGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGGCGCTGAAGTG	3000
Db	1861	GGAAGCAGAGGTCAGGACGATCGGAAGCCAGCGCCGCTGCTGACGTCCAGACTCCG	1920	2941	CGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGGCGCTGAAGTG	3000
QY	1921	CTTCACTCCCAAGCCTGACGGCTGCGGCGATTTGTAACATGACTAGCTCTCTGGGAGC	1980	3001	TCACAGCCTCTTCTGATTTGAGTGTGAGGTGAAACAGCTTCCAGACCGTGTGCAACCACTA	3060
Db	1921	CTTCACTCCCAAGCCTGACGGCTGCGGCGATTTGTAACATGACTAGCTCTCTGGGAGC	1980	3001	TCACAGCCTCTTCTGATTTGAGTGTGAGGTGAAACAGCTTCCAGACCGTGTGCAACCACTA	3060
QY	1981	CAGAACGTTCCCGCAGAAAGAGCGCGCTCACTCAGAGGGTGAAGCACTGTT	2040	3061	CAAGATCCTCCTGCTCAGGCTTACAGGTTTTCAGCATGTGTGCTGCAGCTCCCATTTCA	3120
Db	1981	CAGAACGTTCCCGCAGAAAGAGCGCGCTCACTCAGAGGGTGAAGCACTGTT	2040	3061	CAAGATCCTCCTGCTCAGGCTTACAGGTTTTCAGCATGTGTGCTGCAGCTCCCATTTCA	3120
QY	2041	CAGCGTGTCAACTACGAGCGGCGCGGCGCCGCTCCTGGGCGCTCTGTGTGGG	2100	3121	TCAGCAAGTTTGAAGAACCCACATTTTTCCTGCGCGTCTCTGACACGCGCTCCCT	3180
Db	2041	CAGCGTGTCAACTACGAGCGGCGCGGCGCCGCTCCTGGGCGCTCTGTGTGGG	2100	3121	TCAGCAAGTTTGAAGAACCCACATTTTTCCTGCGCGTCTCTGACACGCGCTCCCT	3180
QY	2101	CTTGGACGATATCCAGAGGCTTGGCGCACCTTCTGCTGCTGCTGCGGCGCCAGGACCC	2160	3181	CTGCTACTCCTCATCTGAAAGCCAAAGACGAGGATGCTGCTGGGGCCAAAGCGCGCGC	3240
Db	2101	CTTGGACGATATCCAGAGGCTTGGCGCACCTTCTGCTGCTGCTGCGGCGCCAGGACCC	2160	3181	CTGCTACTCCTCATCTGAAAGCCAAAGACGAGGATGCTGCTGGGGCCAAAGCGCGCGC	3240
QY	2161	GCGGCTGAGCTGACTTTGTCAAGTGTGATGTGACGGCGGTACGACACCATCCCCCA	2220	3241	CGGCCCTCTGCCCTCCAGGCGCTGCAGTGGCTGTGCCAACCAAGCATTCCTGCTCAGCT	3300
Db	2161	GCGGCTGAGCTGACTTTGTCAAGTGTGATGTGACGGCGGTACGACACCATCCCCCA	2220	3241	CGGCCCTCTGCCCTCCAGGCGCTGCAGTGGCTGTGCCAACCAAGCATTCCTGCTCAGCT	3300
QY	2221	GGACAGGCTCAGGAGGTATCCCGACGATCATCAAAACCCAGAACACGCTACTGCGTGG	2280	3301	GACTGCACACCGTGTACCTTACCTTACCTGCGCTACTCTGGGTCACTCAGGACAGCCAGCGCA	3360
Db	2221	GGACAGGCTCAGGAGGTATCCCGACGATCATCAAAACCCAGAACACGCTACTGCGTGG	2280	3301	GACTGCACACCGTGTACCTTACCTTACCTGCGCTACTCTGGGTCACTCAGGACAGCCAGCGCA	3360
QY	2281	TCGGTATGCGGTGCTCAGAAAGCCGCCATGGGCACGCTCCGCAAGGCTTCAAGAGCCA	2340	3361	GCTGAGTCCGAAGCTCCCGGGGACGAGCTGACTGCTGAGGCGCGACGCCAACCGCGC	3420
Db	2281	TCGGTATGCGGTGCTCAGAAAGCCGCCATGGGCACGCTCCGCAAGGCTTCAAGAGCCA	2340	3361	GCTGAGTCCGAAGCTCCCGGGGACGAGCTGACTGCTGAGGCGCGACGCCAACCGCGC	3420
QY	2341	CGTCTTACCTTGACAGACCTCAGCCGCTACATGCGACAGTTCGTGGCTCAGCTGAGGA	2400	3421	ACTGCCCTCAGACTTCAAGACCATCTTGAGTGTGATGGCCACCGCCACACAGCCAGGCCGA	3480
Db	2341	CGTCTTACCTTGACAGACCTCAGCCGCTACATGCGACAGTTCGTGGCTCAGCTGAGGA	2400	3421	ACTGCCCTCAGACTTCAAGACCATCTTGAGTGTGATGGCCACCGCCACACAGCCAGGCCGA	3480
QY	2401	GACCAACCGCTGAGGATGCGCTGCTCATCGAGCAGAGCTCCTCCTGAAATGAGGCCAG	2460	3481	GAGCAGACACCGACGACCCCTGTACGCGCGGCTCTACGTCCTCAGGAGGAGGGGGGCGC	3540
Db	2401	GACCAACCGCTGAGGATGCGCTGCTCATCGAGCAGAGCTCCTCCTGAAATGAGGCCAG	2460	3481	GAGCAGACACCGACGACCCCTGTACGCGCGGCTCTACGTCCTCAGGAGGAGGGGGGCGC	3540
QY	2461	CAGTGGCTCTTTCAGCTTCTTCTACGCTTCAATGTGCCACACCGCGTGCATCAGGGG	2520	3541	CACACCCAGCGCGCAGCTGGGAGTGTGAGGCTGTGAGTGTGTTGGCCAGGCGCTG	3600
Db	2461	CAGTGGCTCTTTCAGCTTCTTCTACGCTTCAATGTGCCACACCGCGTGCATCAGGGG	2520	3541	CACACCCAGCGCGCAGCTGGGAGTGTGAGGCTGTGAGTGTGTTGGCCAGGCGCTG	3600
QY	2521	CAAGTCTACGTCCAGTGCAGGGATCCCGAGGCGCTCCTCTCCACGCTGCTGTG	2580	3601	CATGTCCGGTGAAGGCTGAGTGTCCGGCTGAGGCTGTGAGGAGTGTCCAGCCAAAGGCT	3660
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Db	1381	 CACAGACCCCGTCGCGCTGCTGAGCTGCTCCGCCACACAGACGCCCTCGGCAGGTGA	1440
Qy	1441	CGGCTTCGTGCGGGCCCTGCCTGCGCGGCTGGTGCCCCCAGAGGCTCTCGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCGTGCGGGCCCTGCCTGCGCGGCTGGTGCCCCCAGAGGCTCTCGGGGCTCCAGGCA	1500
Qy	1501	CAACGAACGCCGTTCCTCAGGAACACCAGAAGTTTCATCTCCCTGGGAAGCATGCCAA	1560
Db	1501	CAACGAACGCCGTTCCTCAGGAACACCAGAAGTTTCATCTCCCTGGGAAGCATGCCAA	1560
Qy	1561	GCTCTCGCTCGAGGCTGACGTGGGAAGATGACGGTGCGGGGACTGCGCTGGCTGGCGCAG	1620
Db	1561	GCTCTCGCTCGAGGCTGACGTGGGAAGATGACGGTGCGGGGACTGCGCTGGCTGGCGCAG	1620
Qy	1621	GAGCCCAAGGGTGGCTGTCTCCGGCCGCAGAGCACCGTCTCGGTGAGGAGATCCTGGC	1680
Db	1621	GAGCCCAAGGGTGGCTGTCTCCGGCCGCAGAGCACCGTCTCGGTGAGGAGATCCTGGC	1680
Qy	1681	CAAGTTCCTGCACGTGGCTGATGAGTGTTACGTCTGAGCTGCTCAGGTCCTCTCTTTTA	1740
Db	1681	CAAGTTCCTGCACGTGGCTGATGAGTGTTACGTCTGAGCTGCTCAGGTCCTCTCTTTTA	1740
Qy	1741	TGTCACGGAGCACGTTTCAAAGAACAGGCTCTTTTACCGGAAGAGTCTCTGGAG	1800
Db	1741	TGTCACGGAGCACGTTTCAAAGAACAGGCTCTTTTACCGGAAGAGTCTCTGGAG	1800
Qy	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCTTGAAGAGGGTGACCTCGGGGAGCTGTC	1860
Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCTTGAAGAGGGTGACCTCGGGGAGCTGTC	1860
Qy	1861	GGAAAGAGAGGTTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCGG	1920
Db	1861	GGAAAGAGAGGTTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCGG	1920
Qy	1921	CTTCATCCCAAGGCTGACGGGCTGCGGCCGATTTGAAACATGGACTACGCTCGTGGAGC	1980
Db	1921	CTTCATCCCAAGGCTGACGGGCTGCGGCCGATTTGAAACATGGACTACGCTCGTGGAGC	1980
Qy	1981	CAGAACTTCGCGAGAGAAAGAGGGCCGAGCTCTCACCTCGAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACTTCGCGAGAGAAAGAGGGCCGAGCTCTCACCTCGAGGGTGAAGGCACTGTT	2040
Qy	2041	CAGCGTGCTCAACTACAGCGGGCGGGCCCGCCCTCTCTGGGGCCCTCTGTGCTGGG	2100
Db	2041	CAGCGTGCTCAACTACAGCGGGCGGGCCCGCCCTCTCTGGGGCCCTCTGTGCTGGG	2100
Qy	2101	CCTGGAGCATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCGGGGCCAGAGCC	2160
Db	2101	CCTGGAGCATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCGGGGCCAGAGCC	2160
Qy	2161	GCCGCTGAGCTGTACTTTGTCGAAGTGGATGTGACGGGCGGTACGACACCATCCCCA	2220
Db	2161	GCCGCTGAGCTGTACTTTGTCGAAGTGGATGTGACGGGCGGTACGACACCATCCCCA	2220
Qy	2221	GGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACACGCTACTGCTGG	2280
Db	2221	GGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACACGCTACTGCTGG	2280
Qy	2281	TCGGTATGCCGTGGTTCAGAAAGGCCGCCATGGCGACGTCCGCAAGGCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCCGTGGTTCAGAAAGGCCGCCATGGCGACGTCCGCAAGGCTTCAAGAGCCA	2340
Qy	2341	CGTCTCTACCTTGACACACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCGAG	2400
Db	2341	CGTCTCTACCTTGACACACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCGAG	2400
Qy	2401	GACCAAGCCGCTGAGGATGCCGTCTCATTCGAGCAGAGCTCTCCCTGAATGAGGCCAG	2460
Db	2401	GACCAAGCCGCTGAGGATGCCGTCTCATTCGAGCAGAGCTCTCCCTGAATGAGGCCAG	2460
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Qy	2521	CAAGTCTCTAGCTCCAGTGCACAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTCTAGCTCCAGTGCACAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG	2580
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Db	2881	GCAGAGGACTACATCCAGCTATGCCGGACCTCCATCAGAGCAGCTCACTCACTTCAACCG	2940
Qy	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTCGGGTCTTCGGGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTCGGGTCTTCGGGCTGAAGTG	3000
Qy	3001	TCACAGCCTGTTCTCGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3060
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Qy	3181	CTGCTACTCCATCTCTGAAGCAAGACGAGGATGTGCTGGGGCCCAAGGGCGCCG	3240
Db	3181	CTGCTACTCCATCTCTGAAGCAAGACGAGGATGTGCTGGGGCCCAAGGGCGCCG	3240
Qy	3241	CGGCCCCCTGCCCCCGAGGCCGTGACGTGGCTGTGCACCAAGCATTTCTGCTCAAGCT	3300
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Qy	3301	GACTCGACACCGTGTCACTACGTGCCACTCTTCGGGTCACTCAGGACAGCCCAAGAGCA	3360
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Qy	3361	GCTGAGTGGAGCTCCCGGGAGCAGCTGACTGTGCCCTGGAGCCCGCAGCAACCCGGC	3420
Db	3361	GCTGAGTGGAGCTCCCGGGAGCAGCTGACTGTGCCCTGGAGCCCGCAGCAACCCGGC	3420
Qy	3421	ACTGCCCTCAGACTTCAAGACCATCCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
Qy	3481	GAGCAGACACAGCAGCCCTGTACGCCGGGCTCTAGCTCCAGGAGGAGGGGGGGCC	3540
Db	3481	GAGCAGACACAGCAGCCCTGTACGCCGGGCTCTAGCTCCAGGAGGAGGGGGGGCC	3540
Qy	3541	CACACCCAGGCCCGCACCCTGGAGTCTCAGGCCCTGAGTGTGTTGCCAGAGCCCTG	3600
Db	3541	CACACCCAGGCCCGCACCCTGGAGTCTCAGGCCCTGAGTGTGTTGCCAGAGCCCTG	3600

QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCAAGGGCT 3660
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RESULT 11

US-08-974-549A-343
; Sequence 343, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
US-08-974-549A-343
Query Match 99.8%; Score 4008.6; DB 3; Length 4037;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4008; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCAGCGCTCGCTCTGCTGCGACGCTGGGAAGCCCTGCGCCCGCCGACCCCGCGATGCC 60
Db 1 GCAGCGCTCGCTCTGCTGCGACGCTGGGAAGCCCTGCGCCCGCCGACCCCGCGATGCC 60
QY 61 GCGCGCTCCCGCTGCGCGACGCTGCGCTCCCTGCTGCGAGCCGCTGCTGCTGCGAGAGTGT 120
Db 61 GCGCGCTCCCGCTGCGCGACGCTGCGCTCCCTGCTGCGAGCCGCTGCTGCTGCGAGAGTGT 120
QY 121 GCGCGCTGCGACGCTTCTGCGCGCCCTGCGCGCCCGCCGAGGCTGCGGCTGCTGCGAGCGG 180
Db 121 GCGCGCTGCGACGCTTCTGCGCGCCCTGCGCGCCCGCCGAGGCTGCGGCTGCTGCGAGCGG 180
QY 181 GGACCCCGCGGCTTTCGCGCGCTGCTGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 GGACCCCGCGGCTTTCGCGCGCTGCTGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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RESULT 14

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; Sequence 173, Application US/08854050

; Patent No. 6261836

; GENERAL INFORMATION:

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; TITLE OF INVENTION: No. 6261836el Telomerase

; NUMBER OF SEQUENCES: 225

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; SOFTWARE: PatentIP Release #1.0, Version #1.30
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; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
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; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029330US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
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; OTHER INFORMATION: /note= "preliminary sequence for
; OTHER INFORMATION: human TRT cDNA insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-854-050-173
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Query Match

Best Local Similarity 95.9%; Score 3849.2; DB 3; Length 4029;

Matches 3955; Conservative 0; Mismatches 53; Indels 9; Gaps 8;

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Db 361 GCTGTGTGACGGGGCCCGGGGGGCCCCCGAGGCCCTTACCACACAGCGTGGCGAGCTA 420
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QY 541 GGCCTCCACAGCTGCGCCTACAGGTGTGGGGCGCGCGCTGTACACAGCTGGCGCTGCCAC 600
Db 541 GGNCTCCAGCTGCGCCTACCAANGTGTGGGGCGCGCGCTGTACCAAGCTGCGCGCTGCNAC 600
QY 601 TCAGGCGCGGCCCCCGCCACACAGCTAGTGGAGCCCGGAAGGCGTCTGGGATCGCAACGGGC 660
Db 601 TCAGGCGCGGCCCCCGCCACACAGCTANVGGA-CCGGAANGGCTTGGGAT-CCAAAGGGC 658
QY 661 CTGGAACCATAGCTCAGGAGGCGGGGTCCCGCTGGGCTGCCAGCCCGGCTGCGAG 720
Db 659 CTGGAACCATAGCTCAGGAGGCGGGGTCCCGCTGGG-CTGGCAGCCCGGCTGCGAG 717
QY 721 GAGCGGGGGGAGTGCACCGCAAGTCTGGGACGGGTCTGGGCCACCGGGGCGAGGAC 840
Db 778 TGCCCCGTGAGCGGAGCGGACCGCGTGTGGCAGGGGTCTTGGGCCACCGCGGAGGAC 837
QY 841 GCGTGGACCGAGTGACCGTGTGTTCTGTGTGGTGTACCTGCCAGACCCCGCGAAGAGC 900
Db 838 GCTTGGACCGAGTGACCGTGTGTTCTGTGTGGTGTACCTGCCAGACCCCGCGAAGAGC 897
QY 901 CACCTCTTTGGAGGTGGCTCTCTGGCAGCGGCACTCCACCCATCCGTGGGCGCGCA 960
Db 898 CACCTCTTTGGAGGTGGCTCTCTGGCAGCGGCACTCCACCCATCCGTGGGCGCGCA 957
QY 961 GCACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAGCGCTGTGCC 1020
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QY 1081 GCCCTCTTCTACTC-AGCTCTCTGAGGCCACGCTGACTGGGCTCGGAGGCTGCTGG 1139
Db 1075 NCCCTCTTCTACTCAATATATCTGAGGCCACGCTGACTTGGGCTTGGGAGGTTCTG 1134
QY 1140 AGACCATTTTCTGGTTCAGGCCCTTGGATGCCAGGAGCTCCCGCAGGTTGCCCGGCC 1199
Db 1135 GAGACANTCTTCTGGTTCCAGGCTTGGATGCCA-GGATTCGCCGAGGTTGCCCGGCC 1193
QY 1200 TGCCCCAGCGCTACTGCGAAATGGGGCCCTGTCTGTGAGAGCTGTCTGGGAACACAGCGC 1259
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QY 1320 CAGCGGCTGTCTGCGCGGAGAGGCCCGAGGGCTCTGTGGGGCCCGCCGAGGAGG 1379
Db 1314 CAGCGGCTGTCTGCGCGGAGAGGCCCGAGGGCTCTGTGGGGCCCGCCGAGGAGG 1373
QY 1380 -ACACAGACCCCGTGGCTGTGAGCTGCTCGCGCAGCAGCAGCCCTGCGAGGTG 1438
|||||

Db 1374 AACACAGACCCCGCTCGCTGTGTGAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGTG 1433
QY 1439 TACGGCTTGTGTGGGCGCTGCTGCGCGGCTGTGTGCCCCCAGGCTCTTGGGGCTCCAGG 1498
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QY 1559 AAGCTCTCGCTGACAGAGCTGACGTGGAAGATGACGCTGCGGAGCTGCGCTGGCTGGCGC 1618
Db 1554 AAGCTCTCGCTGACAGAGCTGACGTGGAAGATGACGCTGCGGAGCTGCGCTGGCTGGCGC 1613
QY 1619 AGGAGCCAGGGGTTGGCTGTGTCCGCCCGCAGACACCGCTCTCCTGAGAGATCCTG 1678
Db 1614 AGGAGCCAGGGGTTGGCTGTGTCCGCCCGCAGACACCGCTCTCCTGAGAGATCCTG 1673
QY 1679 GCCAAGTTCCCTGCACTGCTGATGATGTGTACGCTGCTGAGCTGCTCAGGTCTTTCTTT 1738
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QY 1739 TATGTACGAGACACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1798
Db 1734 TATGTACGAGACACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1793
QY 1799 AGCAAGTTGCAAGATTTGGAATCAGACAGCACATTTGAAGAGGTTGACGCTCGGGAGCTG 1858
Db 1794 AGCAAGTTGCAAGATTTGGAATCAGACAGCACATTTGAAGAGGTTGACGCTCGGGAGCTG 1853
QY 1859 TCGGAAGCAGAGGTCAGCAGCATCGGGAAGCCAGGCGCCGCTGCTACGCTCCAGACTC 1918
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QY 1919 CGCTTCATCCCAAGCCTGACGGGCTGCGCGGCTTGTGAACATGGACTAGCTGCTGGGA 1978
Db 1914 CGCTTCATCCCAAGCCTGACGGGCTGCGCGGCTTGTGAACATGGACTAGCTGCTGGGA 1973
QY 1979 GCCAAGGTTCCCGCAGAGAAAAGGGCCGAGCGTCTCCTCAGAGGTTGAAGCACTG 2038
Db 1974 GCCAAGGTTCCCGCAGAGAAAAGGGCCGAGCGTCTCCTCAGAGGTTGAAGCACTG 2033
QY 2039 TTCAGCTGTCTAACTACGAGCGGCGGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTG 2098
Db 2034 TTCAGCTGTCTAACTACGAGCGGCGGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTG 2093
QY 2099 GGCCTGACGATATCCACAGGGCTTGGCGCACCTTCTGCTGCTGCTGCTGCTGCTGCTG 2158
Db 2094 GGCCTGACGATATCCACAGGGCTTGGCGCACCTTCTGCTGCTGCTGCTGCTGCTGCTG 2153
QY 2159 CCGCGGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTAGGACACCATCCCC 2218
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QY 2219 CAGGACAGGCTCAGGAGGTCATCGCAGCATATCAAAACCCAGAGACACGCTACTGGTG 2278
Db 2214 CAGGACAGGCTCAGGAGGTCATCGCAGCATATCAAAACCCAGAGACACGCTACTGGTG 2273
QY 2279 CGTGGTATGCCGTGTCCAGAGGGCCCGCATGGGACGCTCCCAAGGCGCTTCAAGAGC 2338
Db 2274 CGTGGTATGCCGTGTCCAGAGGGCCCGCATGGGACGCTCCCGCAGGCGCTTCAAGAGC 2333
QY 2339 CAGCTCTTACCTTGACAGACTCCACGCGTACATGCGAGAGTTCGTTGGCTACCTGCAG 2398
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Db 2394 GANACAGCGCGCTGAGGATGCGTGTATCGAGCAGAGCTCTCTCCCTGAATGAGGCC 2453
QY 2459 AGCAGTGGCTCTTTCGAGCTTCTCTACGCTTCTATGTGCCACCGCGCTGCGCATCAGG 2518
Db 2454 AGCAGTGGCTCTTTCGAGCTTCTCTACGCTTCTATGTGCCACCGCGCTGCGCATCAGG 2513

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0202
TELEFAX: (415) 576-0300

TELEFAX: (413) 376-0300
INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs

LENGTH: 4029 base pairs
TYPE: nucleic acid

TYPE: nucleic acid
STRANDEDNESS: single

STRANDEDNESS: single
TOPOLOGY: linear

TOPOLOGY: LINE
MOLECULE TYPE: cDNA

MOLECULE:
FEATURE:

NAME/KEY:

NAME/KEY: 1 4029
LOCATION: 1 4029

LOCATION: 1.4029

OTHER INFORMATION: /note human TPT cDNA insert of

human TRT CDNA ins
plasmid pCBP131⁺

	plasmid pGRN121 ^a	SEQ ID NO: 173.
	SEQUENCE DESCRIPTION:	

US-09-430-323-173
SEQUENCE

Query Match . 95.9%; Score 3849.2; DB 4; Length 4029;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3955; Conservative 0; Mismatches 53; Indels 9; Gaps 8;

Db	1794	AGCAAGTTGCAAGCATTGGAATCAGACAGCACTTTGAAGAGGCTGCAGCTCGGGAGCTG	1853
QY	1859	TCGGGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTC	1918
Db	1854	TCGGGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTC	1913
QY	1919	CGCTTCATCCCAAGCCTGACGGGTGCGGCCGATTGTGAACATGACACTACCTCGTGGA	1978
Db	1914	CGCTTCATCCCAAGCCTGACGGGTGCGGCCGATTGTGAACATGACACTACCTCGTGGA	1973
QY	1979	GCCAGAAGTTCGGCAGAGAAAAGAGGCGGAGCGTCTCACTCGAGGGTGAAGGCACTG	2038
Db	1974	GCCAGAAGTTCGGCAGAGAAAAGAGGCGGAGCGTCTCACTCGAGGGTGAAGGCACTG	2033
QY	2039	TTACGGTGTCAACTACGAGCGGCGGCGGCCCGCCGCTCTCGGGCCCTCTGTGCTG	2098
Db	2034	TTACGGTGTCAACTACGAGCGGCGGCGGCCCGCCGCTCTCGGGCCCTCTGTGCTG	2093
QY	2099	GGCCTGGAGATATCCACAGGGCCTGGCGCACTTTCGTGCTGCGTGTGCGGGCCAGAGAC	2158
Db	2094	GGCCTGGAGATATCCACAGGGCCTGGCGCACTTTCGTGCTGCGTGTGCGGGCCAGAGAC	2153
QY	2159	CGCGCCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGTGACGACACCATCCCT	2218
Db	2154	CGCGCCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGTGACGACACCATCCCT	2213
QY	2219	CAGGACAGCTCAGGAGGTATCGCCAGCATCATCAACCCAGACAGCTACTGCGTG	2278
Db	2214	CAGGACAGCTCAGGAGGTATCGCCAGCATCATCAACCCAGACAGCTACTGCGTG	2273
QY	2279	CGTCGGATGTCGCTGCTCAGAGGCGGCCCATGGCACGTCCGGAAGCCCTTCAAGAGC	2338
Db	2274	CGTCGGATGTCGCTGCTCAGAGGCGGCCCATGGCACGTCCGGAAGCCCTTCAAGAGC	2333
QY	2339	CAGCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACCTGCAG	2398
Db	2334	CAGCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACCTGCAG	2393
QY	2399	GAGACAGCCCTGAGGATCGCTGCTCATCGAGCAGAGCTCTCCCTGATGAGGCC	2458
Db	2394	GANAACAGCCCTGAGGATCGCTGCTCATCGAGCAGAGCTCTCCCTGATGAGGCC	2453
QY	2459	AGCAGTGGCTCTTCACGCTTCTTCATGTCACACACGCCCTGGGCATCAGG	2518
Db	2454	AGCAGTGGCTCTTCACGCTTCTTCATGTCACACACGCCCTGGGCATCAGG	2513
QY	2519	GGCAAGTCTACGTCCAGTCCAGGGATCCCGCAGGGTCCATCTCTCCACGCTGCTC	2578
Db	2514	GGCAAGTCTACGTCCAGTCCAGGGATCCCGCAGGGTCCATCTCTCCACGCTGCTC	2573
QY	2579	TGCAGCCTGCTACGGCAGCATGGAGAACAGCTGTTTCGGGGATTCGGCGGAGCGG	2638
Db	2574	TGCAGCCTGCTACGGCAGCATGGAGAACAGCTGTTTCGGGGATTCGGCGGAGCGG	2633
QY	2639	CTGCTCTCGGTTGGTGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAA	2698
Db	2634	CTGCTCTCGGTTGGTGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAA	2693
QY	2699	ACCTTCTCAGACCCCTGTCGAGGTGCTCCTGAGTATGGTGCTGCTGCTGCTGCTG	2758
Db	2694	ACCTTCTCAGACCCCTGTCGAGGTGCTCCTGAGTATGGTGCTGCTGCTGCTGCTG	2753
QY	2759	ANAGAGTGGTGAATTCCTCTAGNAGACGAGGCCCTGGGTGGCAGGCTTTGTTACAG	2818
Db	2754	ANAGAGTGGTGAATTCCTCTAGNAGACGAGGCCCTGGGTGGCAGGCTTTGTTACAG	2813
QY	2819	ATGCGGGCCACGGCTATTCCTCTGTTGGTGGCTGCTGCTGATACCGGACCTGGAG	2878
Db	2814	ATGCGGGCCACGGCTATTCCTCTGTTGGTGGCTGCTGCTGATACCGGACCTGGAG	2873
QY	2879	GTGCAAGGAGTACTTCCAGCTATGCCCGGACCTCCATCAGAGCCAGCTCTACCTTCAAC	2938
Db	2874	GTGCAAGGAGTACTTCCAGCTATGCCCGGACCTCCATCAGAGCCAGCTCTACCTTCAAC	2933
QY	2939	CGCGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGCTTTGGGGCTGAAG	2998
Db	2934	CGCGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGCTTTGGGGCTGAAG	2993
QY	2999	TGTCACAGCCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGCACCAACATC	3058
Db	2994	TGTCACAGCCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGCACCAACATC	3053
QY	3059	TTACAGATCCTCCTGCTGAGGGGTACAGGTTTACAGATGTGTGCTGAGCTTCCATTT	3118
Db	3054	TACAGATCCTCCTGCTGAGGGGTACAGGTTTACAGATGTGTGCTGAGCTTCCATTT	3113
QY	3119	CATCAGCAAGTTTGAAGAACCACCATTTTCTCGCGTCTATCTCTGACAGGCTCTCC	3178
Db	3114	CATCAGCAAGTTTGAAGAACCACCATTTTCTCGCGTCTATCTCTGACAGGCTCTCC	3173
QY	3179	CTCTGCTACTCCTTGAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCGCC	3238
Db	3174	CTCTGCTACTCCTTGAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCGCC	3233
QY	3239	GGCGGCTCTGCTCCTCCAGGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGTCAAAG	3298
Db	3234	GGCGGCTCTGCTCCTCCAGGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGTCAAAG	3293
QY	3299	CTGACTCGACACCGTGTACCTACGTGCCACTCTGGGCTCACTCAGGACGCCACAGCG	3358
Db	3294	CTGACTCGACACCGTGTACCTACGTGCCACTCTGGGCTCACTCAGGACGCCACAGCG	3353
QY	3359	CAGCTGAGTCCGAAGCTCCCGGGACGAGCTGACTGCCCTGGAGCCCGCAGCAACCCG	3418
Db	3354	CAGCTGAGTCCGAAGCTCCCGGGACGAGCTGACTGCCCTGGAGCCCGCAGCAACCCG	3413
QY	3419	GCATGCTCCTCAGACTTCAAGACCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT	3478
Db	3414	GCATGCTCCTCAGACTTCAAGACCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT	3473
QY	3479	GAGAGCAGACACGAGCAGCCCTGTCACGCGGGCTCTAGTCCCGGAGGGAGGGCGG	3538
Db	3474	GAGAGCAGACACGAGCAGCCCTGTCACGCGGGCTCTAGTCCCGGAGGGAGGGCGG	3533
QY	3539	CCACACCCAGGCGCCAGCGCTGGGAGTCTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGT	3598
Db	3534	CCACACCCAGGCGCCAGCGCTGGGAGTCTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGT	3593
QY	3599	TGATGTCGCGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTGAGGAGG	3658
Db	3594	TGATGTCGCGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTGAGGAGG	3653
QY	3659	CTGAGTGTCCAGCACACTTCCGCTCTCACTTCCCGCAGGCTGCGGCTCCACCC	3718
Db	3654	CTGAGTGTCCAGCACACTTCCGCTCTCACTTCCCGCAGGCTGCGGCTCCACCC	3713
QY	3719	CAGGGCAGCTTTTCTCACCAGGAGCGGCTTCCACTCCCGCAGATAGGAATAGTCCAT	3778
Db	3714	CAGGGCAGCTTTTCTCACCAGGAGCGGCTTCCACTCCCGCAGATAGGAATAGTCCAT	3773
QY	3779	CCCCAGATTGCGCATTTGTCACCCCTCGCCCTCTCTTTGCCCTTCCACCCCGGCT	3838
Db	3774	CCCCAGATTGCGCATTTGTCACCCCTCGCCCTCTCTTTGCCCTTCCACCCCGGCT	3833
QY	3839	CCAGGTGGAGACCTTCAGAGGAGCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTC	3898
Db	3834	CCAGGTGGAGACCTTCAGAGGAGCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTC	3893
QY	3899	TGCGCTGTACACAGGAGGAGCCCTGCACCTGGATGGGCTCTGCTGGGTCAAAATGGG	3958
Db	3894	TGCGCTGTACACAGGAGGAGCCCTGCACCTGGATGGGCTCTGCTGGGTCAAAATGGG	3953
QY	3959	GGGAGTGTGTTGGGAGTAAATACATGAATATATGATGATGATGATGATGATGATGATGAT	4015
Db	3954	GGGAGTGTGTTGGGAGTAAATACATGAATATATGATGATGATGATGATGATGATGATGAT	4010

Search completed: October 15, 2003, 04:40:22
Job time : 241 secs

Db	121	GCCGCTGGCCACAGTTCGTGCGGCGCTGGGGCCCCAGGGCTGGCGCTGGTCAGCGCGG	180
QY	181	GGACCCGGGGCTTCCCGCGCGCTGGTGGCCCAAGTGCCTGGTGGTGGCTGGGACGC	240
Db	181	GGACCCGGGGCTTCCCGCGCGCTGGTGGCCCAAGTGCCTGGTGGTGGCTGGGACGC	240
QY	241	ACGGCGCCCGCCCGCGCGCGCTTCCCTTCGCGCAGGTGTCTCCCTGAAGAGCTGTGTGC	300
Db	241	ACGGCGCCCGCCCGCGCGCGCTTCCCTTCGCGCAGGTGTCTCCCTGAAGAGCTGTGTGC	300
QY	301	CCGAGTGTGCAGAGGCTGTGGCAGCGCGCGCGCGCGAGAACAGTGTCTGGCTTCGC	360
Db	301	CCGAGTGTGCAGAGGCTGTGGCAGCGCGCGCGCGCGAGAACAGTGTCTGGCTTCGC	360
QY	361	GCTGCTGGACGGGGCCCGGGGGCCCCCGCGAGGCTTCACACACAGCGTGCAGCTA	420
Db	361	GCTGCTGGACGGGGCCCGGGGGCCCCCGCGAGGCTTCACACACAGCGTGCAGCTA	420
QY	421	CGTGCCCAACAGGTGTACCGACGCTGTGGGGGAGCGGGGCTGGGGCTGCTGCTGC	480
Db	421	CGTGCCCAACAGGTGTACCGACGCTGTGGGGGAGCGGGGCTGGGGCTGCTGCTGC	480
QY	481	CGCGTGGCGGACGACGTGTCTGGTTCACCTGCTGCGACGCTGCGCGCTTGTGTGTGT	540
Db	481	CGCGTGGCGGACGACGTGTCTGGTTCACCTGCTGCGACGCTGCGCGCTTGTGTGTGT	540
QY	541	GGCTCCCAAGCTCGCGCTTACCAAGGTGTGGGGCGCGCGCTGTACCAAGCTGGCGCT	600
Db	541	GGCTCCCAAGCTCGCGCTTACCAAGGTGTGGGGCGCGCGCTGTACCAAGCTGGCGCT	600
QY	601	TCAGCGCGCGCGCGCGCGCGCTGTAGTGACCGCGCGCGCTGTGGATGCGAACGGCG	660
Db	601	TCAGCGCGCGCGCGCGCGCGCTGTAGTGACCGCGCGCGCTGTGGATGCGAACGGCG	660
QY	661	CTGAACCATAGCTGTAGGAGGCGCGCGCTGTGGATGCGAACGGCGCTGTGGATGCG	720
Db	661	CTGAACCATAGCTGTAGGAGGCGCGCGCTGTGGATGCGAACGGCGCTGTGGATGCG	720
QY	721	GAGCGCGGGGCGCGCGCGCGCTGTGGATGCGAACGGCGCTGTGGATGCGAACGGCG	780
Db	721	GAGCGCGGGGCGCGCGCGCGCTGTGGATGCGAACGGCGCTGTGGATGCGAACGGCG	780
QY	781	TGCGCCCTGAGCGGAGGCGCGCGCTGTGGATGCGAACGGCGCTGTGGATGCGAAC	840
Db	781	TGCGCCCTGAGCGGAGGCGCGCGCTGTGGATGCGAACGGCGCTGTGGATGCGAAC	840
QY	841	CGGTGGACCGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
Db	841	CGGTGGACCGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
QY	901	CACCTCTTTGAGGGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
Db	901	CACCTCTTTGAGGGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
QY	961	GCACCGCGGGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1020
Db	961	GCACCGCGGGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1020
QY	1021	CCCGGTGTAGCGGAGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1080
Db	1021	CCCGGTGTAGCGGAGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1080
QY	1081	GCCT	1140
Db	1081	GCCT	1140
QY	1141	GACCATCTTCTTGGTTCAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1200
Db	1141	GACCATCTTCTTGGTTCAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1200
QY	1201	GCCT	1260
Db	1201	GCCT	1260
QY	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGACCTGCCGCTGGAGCTGGGTCACCCAGC	1320
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGACCTGCCGCTGGAGCTGGGTCACCCAGC	1320
QY	1321	AGCCGGTGTCTGTGTCGCCGGGAGAACCCAGGGCTGTGTGGGGCCCCCGAGGAGGA	1380
Db	1321	AGCCGGTGTCTGTGTCGCCGGGAGAACCCAGGGCTGTGTGGGGCCCCCGAGGAGGA	1380
QY	1381	CACAGACCCCGCTGCCCTGGTGCAGCTGCTCCCGCAGCACACAGCCCTTGGGCTGTA	1440
Db	1381	CACAGACCCCGCTGCCCTGGTGCAGCTGCTCCCGCAGCACACAGCCCTTGGGCTGTA	1440
QY	1441	CGGCTTGTGGGGGCTGCCCTGGTGCAGCTGCTCCCGCAGCACACAGCCCTTGGGCTG	1500
Db	1441	CGGCTTGTGGGGGCTGCCCTGGTGCAGCTGCTCCCGCAGCACACAGCCCTTGGGCTG	1500
QY	1501	CAACGAACCGCGCTTCCCTCAGGAACACCAAGATTCATCTCCCTGGGAGAGATGCCAA	1560
Db	1501	CAACGAACCGCGCTTCCCTCAGGAACACCAAGATTCATCTCCCTGGGAGAGATGCCAA	1560
QY	1561	GCTCTGCTGAGGAGCTGACCTGGAAGATGAGCGTGGGAGTGCCTTGGCTGGCGAG	1620
Db	1561	GCTCTGCTGAGGAGCTGACCTGGAAGATGAGCGTGGGAGTGCCTTGGCTGGCGAG	1620
QY	1621	GAGCCAGGGGTTGGCTGTGTTCGGCGCAGAGCACCGTCTGGTGGAGATCTTGGC	1680
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QY	1681	CAAGTTCCTGACCTGGCTGTGTGTTCGGCGCAGAGCACCGTCTGGTGGAGATCTTGGC	1740
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QY	1741	TGTACGAGAGACCGTTCCTCAAGACAGAGCTCTTTTCTACCGGAGAGTGTCTGGAG	1800
Db	1741	TGTACGAGAGACCGTTCCTCAAGACAGAGCTCTTTTCTACCGGAGAGTGTCTGGAG	1800
QY	1801	CAAGTTCGAAGACATTTGAATCAGACGACCTTGAAGAGGCTGAGCTGGGAGCTGC	1860
Db	1801	CAAGTTCGAAGACATTTGAATCAGACGACCTTGAAGAGGCTGAGCTGGGAGCTGC	1860
QY	1861	GGAGCAGAGCTCAGGAGCATCGGAGAGCCAGCGCGCGCTGTGAGCTCCAGACTCCG	1920
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QY	1921	CTTCATCCCAAGCTGACGGCTGCGCGCGCTGTGAAATGAGCTACGTCGTTGGAGC	1980
Db	1921	CTTCATCCCAAGCTGACGGCTGCGCGCGCTGTGAAATGAGCTACGTCGTTGGAGC	1980
QY	1981	CAGAACCTTCGCGAGAGAAAGAGGCGCGCGCTGTGAGCTGAGGCTGAGGCTGTT	2040
Db	1981	CAGAACCTTCGCGAGAGAAAGAGGCGCGCGCTGTGAGCTGAGGCTGAGGCTGTT	2040
QY	2041	CAGCGTCTCAACTACGAGCGCGCGCGCTGTGAGCTGAGGCTGAGGCTGTT	2100
Db	2041	CAGCGTCTCAACTACGAGCGCGCGCGCTGTGAGCTGAGGCTGAGGCTGTT	2100
QY	2101	CTTGGAGATATCCAGAGGCTTGGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	2160
Db	2101	CTTGGAGATATCCAGAGGCTTGGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	2160
QY	2161	GCCTCTGAGCTGACTTGTCAAGTGTGATGTGACGGGCGCTGTGAGCTGCTGCTGCTG	2220
Db	2161	GCCTCTGAGCTGACTTGTCAAGTGTGATGTGACGGGCGCTGTGAGCTGCTGCTGCTG	2220
QY	2221	GGAGAGCTCAGGAGCTATCCGACATCATCAAAACCCAGAACACGCTGCTGCTGCTG	2280
Db	2221	GGAGAGCTCAGGAGCTATCCGACATCATCAAAACCCAGAACACGCTGCTGCTGCTG	2280
QY	2281	TCGGTATGCGTGTCCAGAGGCGCGCGCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTG	2340
Db	2281	TCGGTATGCGTGTCCAGAGGCGCGCGCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTG	2340

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QY 2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTTGGCTCACTGCGAGGA 2400
DB 2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTTGGCTCACTGCGAGGA 2400
QY 2401 GACCAAGCCGCTGAGGAGTCCGCTCATGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
DB 2401 GACCAAGCCGCTGAGGAGTCCGCTCATGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
QY 2461 CAGTGGCCCTCTTGGAGCTTCTCTACGCTTCAATGTCACACCGCGTGGCATCAGGGG 2520
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QY 2521 CAAAGTCTACCTCCAGTCCAGGGGATCCGAGGGCTCCATCTCCACCGTGTCTG 2580
DB 2521 CAAAGTCTACCTCCAGTCCAGGGGATCCGAGGGCTCCATCTCCACCGTGTCTG 2580
QY 2581 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGCGGGATTCGGCGGACGGCT 2640
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DB 2641 GCTCCTGCGTTTGGTGGAATTTCTTGTGTTGACACCTCACTCACCACCGCGAAAC 2700
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DB 2701 CTTCTCAGGACCCCTGGTCCGAGGTGCTCCTGAGTATGGCTGGTGAACCTTGGGAA 2760
QY 2761 GACAGTGGTGAATTCCTCTGTAGAAGCAGGCGCTGGTGGCAGCGCTTTTCTCAGAT 2820
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DB 2821 GCCGGCCACGGCCTATTCCCTGTGTGCGCCTGCTGCTGGATACCCGACCCCTGGAGT 2880
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DB 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGCCCTCCCT 3180
QY 3181 CTGCTACTCCATCTGAAAGCAAGCAAGCAGGAGTGTGCTGGGGGCCAAGGGCCCGC 3240
DB 3181 CTGCTACTCCATCTGAAAGCAAGCAAGCAGGAGTGTGCTGGGGGCCAAGGGCCCGC 3240
QY 3241 CGGCCCCCTGCCCCCGAGCGCGTGCAGTGGCTGTGCCAACAAGCATTTCTGCTCAAGCT 3300
DB 3241 CGGCCCCCTGCCCCCGAGCGCGTGCAGTGGCTGTGCCAACAAGCATTTCTGCTCAAGCT 3300
QY 3301 GACTCGACACCGGTGCTCAGTGCCTCTGCTGGGTCACTCAGGACAGCCCGCAGCGCA 3360
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QY 3361 GCTGAGTCGGAAGTCTCCCGGGACGACGCTGACTGCTTGGAGGCGCGACGCCCGG 3420
DB 3361 GCTGAGTCGGAAGTCTCCCGGGACGACGCTGACTGCTTGGAGGCGCGACGCCCGG 3420
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DB 3481 GAGCAGACACACAGCCCTGTACGCCGGCTCTAGTCCAGGAGGAGGAGGCGGCC 3540
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DB 3541 CACACCCAGGCGCCGCTGAGTGTGAGGCGCTTCACTGAGTGTGTTGGCCGAGGCGTG 3600
QY 3601 CATGTCCGCTGAAGCTGAGTGTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCT 3660
DB 3601 CATGTCCGCTGAAGCTGAGTGTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCT 3660
QY 3661 GAGTGTCCAGCACACCTGCTTCACTTCCACAGGCTGCGCTGCGCTCCACCCCA 3720
DB 3661 GAGTGTCCAGCACACCTGCTTCACTTCCACAGGCTGCGCTGCGCTCCACCCCA 3720
QY 3721 GGCCAGCTTTTCTCACCAGGAGCGCGCTTCCACTCCACACATAGGAATAGTCCATCC 3780
DB 3721 GGCCAGCTTTTCTCACCAGGAGCGCGCTTCCACTCCACACATAGGAATAGTCCATCC 3780
QY 3781 CCAGATTCGCCATTTTCAACCCCTGCGCTGCGCTTCTTTCCTTCCACCCCAACATCC 3840
DB 3781 CCAGATTCGCCATTTTCAACCCCTGCGCTGCGCTTCTTTCCTTCCACCCCAACATCC 3840
QY 3841 AGTGAGAGCCCTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
DB 3841 AGTGAGAGCCCTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
QY 3901 CCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
DB 3901 CCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
QY 3961 GAGTGTCTGGGAGTAAATATCTGAATATATAGTGTTCAGTTCAGTTTGAAGAAA 4015
DB 3961 GAGTGTCTGGGAGTAAATATCTGAATATATAGTGTTCAGTTCAGTTTGAAGAAA 4015
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RESULT 2

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US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1
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Query Match 100.0%; Score 4015; DB 10; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCGCTGCTGCTGCTGCGCAGCTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCC 60
DB 1 GCAGCGCTGCTGCTGCTGCGCAGCTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCC 60
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Qy		61	GC	CGCTCC	CCCCGTCGCGAGCCTGTGCTCCCTGCTGCGACGCCACTACCGAGTGCT	120
Db		61	GC	CGCTCC	CCCCGTCGCGAGCCTGTGCTCCCTGCTGCGACGCCACTACCGAGTGCT	120
Qy		121	GC	CGCTGG	CACCTTGGTGGCGCTGAGSGCCCAGGCGTGGCGCTGGTGCAGCGCG	180
Db		121	GC	CGCTGG	CACCTTGGTGGCGCTGAGSGCCCAGGCGTGGCGCTGGTGCAGCGCG	180
Qy		181	GG	ACC	GGGGGCTTTCCGGCGCTGTGGGCCCAAGTAGTGCCTGGTGGCTGAAGAGCTGTGGC	240
Db		181	GG	ACC	GGGGGCTTTCCGGCGCTGTGGGCCCAAGTAGTGCCTGGTGGCTGAAGAGCTGTGGC	240
Qy		241	AC	GCGCGCC	CCCCCGCGCCCTTCTTCGCCCAGAGTGCTCGCTTGGCGCTGGCGCTGGCG	300
Db		241	AC	GCGCGCC	CCCCCGCGCCCTTCTTCCGCCAAGTGCTCGCTTAAAGAGAGTGGTGGC	300
Qy		301	CC	GAGTGT	CGCAGAGCTGTGCGAGCGCGCGGAGAAGTGCTCGCTTGGCGCTTGGCTTCGC	360
Db		301	CC	GAGTGT	CGCAGAGCTGTGCGAGCGCGCGGCGAAGACGTGCTGGCTTGGCTTCGC	360
Qy		361	GT	CTGTGG	AGGGGGCCCGCGGGGGCCCCCGGAGGCTTCAACACAGGCTGCGCAGCTA	420
Db		361	GT	CTGTGG	AGGGGGCCCGCGGGGGCCCCCGGAGGCTTCAACACAGGCTGCGCAGCTA	420
Qy		421	CT	TGCCCAA	CACGGTGACCGACGACGCTGCGGGGAGCGGGGCTGTGTGTGGG	480
Db		421	CT	TGCCCAA	CACGGTGACCGACGACGCTGCGGGGAGCGGGGCTGTGTGTGGG	480
Qy		481	CC	CGTGGG	CGACGCTGTGCTTACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT	540
Db		481	CC	CGTGGG	CGACGCTGTGCTTACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT	540
Qy		541	GG	CTCCAG	TGCGCCTTACCAGTGTGCGGGCGCGCGCTTACACAGCTCGCGCGCTGCCAC	600
Db		541	GG	CTCCAG	TGCGCCTTACCAGTGTGCGGGCGCGCGTGTACACAGCTCGCGCGCTGCCAC	600
Qy		601	TC	AGGCCCC	CGCCCGCCACACGCTAGTGACCCCGAAGCGTCTGGATGCGAACGGG	660
Db		601	TC	AGGCCCC	CGCCCGCCACACGCTAGTGACCCCGAAGCGTCTGGATGCGAACGGG	660
Qy		661	CT	GAAACA	TAGGTCAGGAGGCGGGGTCCCGCTGGGCTGCCAGCCCGGGTGCAG	720
Db		661	CT	GAAACA	TAGGTCAGGAGGCGGGGTCCCGCTGGGCTGCCAGCCCGGGTGCAG	720
Qy		721	GAG	CGCGGG	GCAGTGCCAGCGTAAGTCTGCGCTTCCCAAGAGCGCCAGCGCTGGCGC	780
Db		721	GAG	CGCGGG	GCAGTGCCAGCGTAAGTCTGCGCTTCCCAAGAGCGCCAGCGCTGGCGC	780
Qy		781	TG	CCCC	TGAGCGGAGCGGAGCCGCTTGGGCGAGGGTCTCGGGCCACCCGGCGAGGAC	840
Db		781	TG	CCCC	TGAGCGGAGCGGAGCCGCTTGGGCGAGGGTCTCGGGCCACCCGGCGAGGAC	840
Qy		841	GC	GTGAC	CGAGTGACCGTGTCTCTGTGTGTACCTGCCAGACCCGCCGAAGAAGC	900
Db		841	GC	GTGAC	CGAGTGACCGTGTCTCTGTGTGTACCTGCCAGACCCGCCGAAGAAGC	900
Qy		901	CA	CTCTTT	TGAGGGTGGCTCTGTGGACCGCGCACTCCACCCTCCGTGGCGCGCCA	960
Db		901	CA	CTCTTT	TGAGGGTGGCTCTGTGGACCGCGCACTCCACCCTCCGTGGCGCGCCA	960
Qy		961	GC	ACCAG	CGGGCCCCCATCCAAATCGCGGCCACACGTCCTGTGGGACAGCGCTGTGTC	1020
Db		961	GC	ACCAG	CGGGCCCCCATCCACATCGCGGCCACACGTCCTGTGGGACAGCGCTGTGTC	1020
Qy		1021	CC	CGGTGT	ACGCCAGACCAAGCACTTCTACTCTCAGGGGACAAAGAGCAGCTGGC	1080
Db		1021	CC	CGGTGT	ACGCCAGACCAAGCACTTCTACTCTCAGGGGACAAAGAGCAGCTGGC	1080
Qy		1081	GCC	CTCTCT	CTACTCAGCTCTCTGAGGCGCCAGCGCTGACTGGGCTCGGAGGCTCGTGA	1140
Db		1081	GCC	CTCTCT	CTACTCAGCTCTCTGAGGCGCCAGCGCTGACTGGGCTCGGAGGCTCGTGA	1140
Qy		1141	GAC	ATCTTT	CTGGGTTCCAGGGCCCTGGATGCCAGGACACTCCCGCAGGTTGCCCGCGCT	1200

Db	1141	GACCACTTCTTGGGTTCCAGGCCCTTGAGTCAGGAGACTCCCAGCAGGTGCCCCGCCT	1200
Qy	1201	GCCCCAGCGCTACTGGCAAATCGGCCCTTGTTCTTGAGACTGCTTTGGGAACAACACACGCGA	1260
Db	1201	GCCCCAGCGCTACTGCAAAATGGGCCCTGTGTTCTTGAGACTGCTTTGGGNAACACACGCGCA	1260
Qy	1261	GTGCCCCCTACGGGGTGCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTACACCACAGC	1320
Db	1261	GTCCCCCTACGGGGTGCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTACACCACAGC	1320
Qy	1321	AGCCGTGCTGTGCCCCGGAGAACCCACAGSGCTCTGTGGCGGCCCCCGAGAGAGGA	1380
Db	1321	AGCCGTGCTGTGCCCCGGAGAACCCACAGSGCTCTGTGGCGGCCCCCGAGAGAGGA	1380
Qy	1381	CACAGACCCCGCTGCGCTGCTGTCAGCTGTCTCCGCCACAGCACAGCAGCCCTTGGCAGGTGA	1440
Db	1381	CACAGACCCCGCTGCGCTGCTGTCAGCTGTCTCCGCCACAGCACAGCAGCCCTTGGCAGGTGA	1440
Qy	1441	CGGCTTGTGCGGGCTGCCTCGCGCGGTGTCGCCCGAGGCTCTGCGGCTCCAGGCA	1500
Db	1441	CGGCTTGTGCGGGCTGCCTCGCGCGGTGTCGCCCGAGGCTCTGCGGCTCCAGGCA	1500
Qy	1501	CACGAAACCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGNAAGCATGCCAA	1560
Db	1501	CACGAAACCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGNAAGCATGCCAA	1560
Qy	1561	GCCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGC GGACTGCGCTTGGCTGGCGCAG	1620
Db	1561	GCCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGC GGACTGCGCTTGGCTGGCGCAG	1620
Qy	1621	GAGCCAGGGGTTGGTGTTCCGCGCCGACAGCACCGCTCGTGGAGAGATCCTGGC	1680
Db	1621	GAGCCAGGGGTTGGTGTTCCGCGCCGACAGCACCGCTCGTGGAGAGATCCTGGC	1680
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Db	1681	CAAGTTCTGCACCTGGCTGATGATGTGTACGTCTGTCGAGCTGCTCAGGTCTTCTTTTA	1740
Qy	1741	TGTCAGGGACCAACGTTTTCAAAGAACAAGCTCTTTTTTACCGGAAGAGTGTCTGGAG	1800
Db	1741	TGTCAGGGACCAACGTTTTCAAAGAACAAGCTCTTTTTTACCGGAAGAGTGTCTGGAG	1800
Qy	1801	CAAGTGTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTCGGGAGCTGTC	1860
Db	1801	CAAGTGTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTCGGGAGCTGTC	1860
Qy	1861	GGAGCAGAGGTGAGCAGCATCGGAAGCCAGSCCGCCCTGCTGACGTCCAGACTCCG	1920
Db	1861	GGAGCAGAGGTGAGCAGCATCGGAAGCCAGSCCGCCCTGCTGACGTCCAGACTCCG	1920
Qy	1921	CTTCATCCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGACTACCTCGTGGGAGC	1980
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGACTACCTCGTGGGAGC	1980
Qy	1981	CAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
Qy	2041	CAGGCTGCTCAACTACAGCGGGCGGGCCCGGGCTCCTGGGCGCTCTGTGCTGGG	2100
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Db	2101	CTTGAGCATATCCACAGGCGCTGGCGACCTCTGCTGCTGCTGGCGCCAGGACCC	2160
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Db	2161	GC CGCTGAGCTGTACTTTGTC AAGGTGATGTGACGGGCGGTACGACACCATCCCCCA	2220
Qy	2221	GGACGCGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2280
Db	2221	GGACGCGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2280

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Db 2281 TCGGTATGCGGTGGTCAGAAAGCGCCCATGCGCAGTCCGCAAGGCCCTTCAAGAGCCA 2340
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Db 3961 GAGTGTCTGTTGGAGTAAATATGATATGATGATGATGATGATGATGATGATGATGATGAT 4015

RESULT 3

US-09-843-676-224

; Sequence 224, Application US/09843676

; Patent No. US20020164786A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20020164786A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

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Db	1621	GAGCCAGAGGTTGGCTGTGTTCCGGCCGAGACACCGTCTCCGTGAGAGATCTCGGC	1680
QY	1681	CAAGTTCCTGCACTGCTGATGAGTGTGTACGTCGTCGAGCTCTCAGGCTCTTCTTTTA	1740
Db	1681	CAAGTTCCTGCACTGCTGATGAGTGTGTACGTCGTCGAGCTCTCAGGCTCTTCTTTTA	1740
QY	1741	TGTACGAGAGACACCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
Db	1741	TGTACGAGAGACACCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
QY	1801	CAAGTTCGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGTCAGCTGGGGAGTGTG	1860
Db	1801	CAAGTTCGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGTCAGCTGGGGAGTGTG	1860
QY	1861	GGAAGCAGAGGTCAGCAGCATCGGAAGCCAGGCGCCCTGCTGACGTCGAGACTCCG	1920
Db	1861	GGAAGCAGAGGTCAGCAGCATCGGAAGCCAGGCGCCCTGCTGACGTCGAGACTCCG	1920
QY	1921	CTTTCATCCCAAGCCTGACGGGCTGGCGGATTTGTGAACATGGACTACGTCCTGGGAGC	1980
Db	1921	CTTTCATCCCAAGCCTGACGGGCTGGCGGATTTGTGAACATGGACTACGTCCTGGGAGC	1980
QY	1981	CAGACGTTCCCGCAGAGAAAGAGCGCCGAGCGTCTACCTCAGAGGTGAAGCACTGTT	2040
Db	1981	CAGACGTTCCCGCAGAGAAAGAGCGCGAGCGTCTCACCTCAGAGGTGAAGCACTGTT	2040
QY	2041	CAGCGTCTCACTAGAGGGGCGCGCGCCCGCCCTCTGGGGCCCTCTGTGTGGG	2100
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QY	2101	CTTGGACGATATCCACAGGCGCTTGGCGCACCTTCTGCTGCTGCTGGCGCCACGAGACC	2160
Db	2101	CTTGGACGATATCCACAGGCGCTTGGCGCACCTTCTGCTGCTGCTGGCGCCACGAGACC	2160
QY	2161	GCGCCTGAGCTGACTTTGTCGAAGGTGGATGTGACGGGCGCGTACGACACCATCCGCCA	2220
Db	2161	GCGCCTGAGCTGACTTTGTCGAAGGTGGATGTGACGGGCGCGTACGACACCATCCGCCA	2220
QY	2221	GGACAGGCTCACGAGGTATCCAGAGCCGCCATGCGGCACGTCGCGCAAGGCCCTTCAAGAGCCA	2280
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QY	2281	TCGGTATGCGGTGGTCCAGAGCCGCCATGCGGCACGTCGCGCAAGGCCCTTCAAGAGCCA	2340
Db	2281	TCGGTATGCGGTGGTCCAGAGCCGCCATGCGGCACGTCGCGCAAGGCCCTTCAAGAGCCA	2340
QY	2341	CGTCTCTACCTTACAGACCTCAGCGGTACATGCGACAGTTCGTCGCTCACCCTGACGGA	2400
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QY	2401	GACACGCCCTGAGGGATGCCCTGCTCATCGAGCAGAGCTCCCTGTAATGAGGCCAG	2460
Db	2401	GACACGCCCTGAGGGATGCCCTGCTCATCGAGCAGAGCTCCCTGTAATGAGGCCAG	2460
QY	2461	CAGTGGCCTCTTCCAGCTCTTCTACGCTTCATGTGCCACGCGGTGCGCATCAGGGG	2520
Db	2461	CAGTGGCCTCTTCCAGCTCTTCTACGCTTCATGTGCCACGCGGTGCGCATCAGGGG	2520
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Db	2521	CAAGTCTAGCTCAGTCCAGGGGATCCCGCAGGGGTCCCTCTCCACGCTGTCTG	2580
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QY	2821	GCCGGCCACAGGCGCTATTCCCTTGGTGGCGCTGCTGCTGATACCCGACCCCTGGAGGT	2880
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QY	2881	GCAGAGGACTACTCAGCTATGCCCGGACCTCCATCAGAGCAGTCTCACCCTTCAACCG	2940
Db	2881	GCAGAGGACTACTCAGCTATGCCCGGACCTCCATCAGAGCAGTCTCACCCTTCAACCG	2940
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Db	3001	TCACAGCCTGTTTCTGGATTTCAGAGTGAACAGAGCTCCACAGCGTGTGACCAACATCTA	3060
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QY	3121	TCAGCAAGTTTGGNAGNACCCACATTTTTCCTGCGGCTCATCTCTGACAGGCGCTCCCT	3180
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QY	3241	CGGCGCTCTGCCCTCAGAGCGCGTGCAGTGGCTGTGCCAACAAAGCATTTCTGTCTCAAGCT	3300
Db	3241	CGGCGCTCTGCCCTCAGAGCGCGTGCAGTGGCTGTGCCAACAAAGCATTTCTGTCTCAAGCT	3300
QY	3301	GACTCGACACCGTGTACCTACGTGCCACCTCTCTGGGCTCTCAGGACAGCCAGAGCGCA	3360
Db	3301	GACTCGACACCGTGTACCTACGTGCCACCTCTCTGGGCTCTCAGGACAGCCAGAGCGCA	3360
QY	3361	GCTGAGTCTGGAAGCTCCCGGGGAGCGCTGCTGCTGGAGCCGCGCAGCCACCCGCGC	3420
Db	3361	GCTGAGTCTGGAAGCTCCCGGGGAGCGCTGCTGCTGGAGCCGCGCAGCCACCCGCGC	3420
QY	3421	ACTGCGCTCAGACTTCAAGACCATCTCTGGACTGTGAGCCACCCGCGCAGCCAGGCGCA	3480
Db	3421	ACTGCGCTCAGACTTCAAGACCATCTCTGGACTGTGAGCCACCCGCGCAGCCAGGCGCA	3480
QY	3481	GAGCAGACACAGCAGCGCTGTCCACGCGGCTCTACGTCCTCCAGGGAGGCGGCGCC	3540
Db	3481	GAGCAGACACAGCAGCGCTGTCCACGCGGCTCTACGTCCTCCAGGGAGGCGGCGCC	3540
QY	3541	CACACCCAGCCCGCAGCGCTGGGAGTCTGAGGCGCTGAGTGTGTTTGGCCAGGCGCTG	3600
Db	3541	CACACCCAGCCCGCAGCGCTGGGAGTCTGAGGCGCTGAGTGTGTTTGGCCAGGCGCTG	3600
QY	3601	CATGTCCGGCTGAAGGCTGAGTGTCCCGCTGAGGCGCTGAGGCGCTGTCAGCCCAAGGCT	3660
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCCGCTGAGGCGCTGAGGCGCTGTCAGCCCAAGGCT	3660
QY	3661	GAGTGTCCACACACCTTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
Db	3661	GAGTGTCCACACACCTTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
QY	3721	GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTTCCCCACATAGGAATAGTCCATCC	3780
Db	3721	GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTTCCCCACATAGGAATAGTCCATCC	3780

QY	721	GAGCGCGGGGCGAGTGCACGCCGAAGTCTGCGGTTGCCCAAGAGGCCACAGCGTGGCGC	780	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
Db	721	GAGCGCGGGGCGAGTGCACGCCGAAGTCTGCGGTTGCCCAAGAGGCCACAGCGTGGCGC	780	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
QY	781	TGCGCCCTGAGCGGAGCGAGCGCCGCTTGCGCAGGGGTCTCTGGGCCACCCGGGCGAGGAC	840	1861	GGAAGCAGAGGTGACGAGCATCGGAAGCCAGGCCCGCCCTGCTGACGFTCCAGACTCCG	1920
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QY	1021	CCGGGTGACGGCGAGACCAAGCACTTCTCTACTCTCCTCAGCGACAAAGAGCAGCTGCG	1080	2101	CTTGGACGATATCCACAGGSCCTGGCGCACCTTCTGCTGCTGTGTGGGGCCCGCAGGACCC	2160
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Db	1141	GACCATCTTCTGGGTTCAGGCGCTGGATGCCAGGAGCTTCCCGCAGGTTGCCCGCCCT	1200	2221	GGACAGGCTCACGAGGTCATGCCAGCATCATCAACCCAGAACACGFTACGTGCGTGG	2280
QY	1201	GCCCCAGCGCTACTGCAAAATCGGCCCTGTTTCTTGAGCTGCTTGGGAACACACGCGCA	1260	2281	TCGGTATGCGGTGCTCAGAAAGCGGCCATGCGCACGTCCGCAAGGCCCTTCAAGAGCCA	2340
Db	1201	GCCCCAGCGCTACTGCAAAATCGGCCCTGTTTCTTGAGCTGCTTGGGAACACACGCGCA	1260	2281	TCGGTATGCGGTGCTCAGAAAGCGGCCATGCGCACGTCCGCAAGGCCCTTCAAGAGCCA	2340
QY	1261	GTGCGCCTACGGGGTGCCTCTCAAGACGACTGCGCGCTGCGAGCTGCGGTTCACCCGAGC	1320	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATCGGACATTCGTGGCTCACCTGCAGGA	2400
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QY	1321	AGCGGTGCTGTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGCAGGAGGAGGA	1380	2401	GACACGCCCTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCTGATGAGGCGCAG	2460
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QY	1381	CACAGACCCCGTGCCTGGTGCAGTGTCTCCGCCAGCAGCAGAGCCCTTGGCAGGTGTA	1440	2461	CAGTGGCTCTTTCAGCTCTTCTTGTGGTGACACCTCAGCTCACCACCGCGAAGAAC	2520
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QY	1681	CAAGTTCCTGCACTGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCTTCTTTTA	1740	2761	GACAGTGGTGAACCTTCCCTGCTAGAACAGAGGCCCTGGGTGGCACGCGCTTGTTCAGAT	2820
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; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
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; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/846,017
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; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
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; INFORMATION FOR SEQ ID NO: 224:
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; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTERT"
; /note= "human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224

Query Match 100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY		61	GGCGCTCCCGCTGCCAGCGTGCCTTCCCTGCTGCGCAGCCACTACCGGAGTGCT	120		1141	GACCATCTTTCTGGGTTCCAGGCCCTTGATGCCAGGACTCCCGCAGGTTGCCCGGCT	1200
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QY		541	GGCTCCCAAGCTGCGCTTACAGGTGTGGGGCGCGCTGTACCAAGCTGGGGCTGCC	600		1621	GAGCCAGGGGTGGCTGTTCCGGCCGACAGACACCTCTCGCTGAGAGATCCTGCG	1680
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; NAME/KEY: CDS
; LOCATION: (35)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

Query Match      100.0%; Score 4015; DB 14; Length 4015;
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QY	1501	CAAGAAAGCCGCTTCTTCAGGAACACCAAGAAATTCATCTCCCTGGGGAAGCATGCCAA	1560		2581	CAGCTCTGTCTACGCGGACATGGAGAACAGCTCTTTTCGGGGGATTCGGCGGGAGCT	2640	
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QY	1561	GCTCTCTGTCTACGAGCTGAGTGGAGATGAGCGTGGGAGCTGGCTGGCTGGCTGGCTGG	1620		2641	GCTCTCTGGTGGTGGATGATTTCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2700	
Db	1561	GCTCTCTGTCTACGAGCTGAGTGGAGATGAGCGTGGGAGCTGGCTGGCTGGCTGGCTGG	1620		2701	CTTCTCTCAGGACCTGGTCCGAGGTGCTCCGAGTATGGTGGTGGTGGTGGTGGTGGTGG	2760	
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; Publication No. US2003005978A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US2003005978A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTERT"
; /note= "human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-611-224

Query Match 100.0%; Score 4015; DB 14; Length 4015;
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Db	1141		1200
		GACCATCTTCTGGTTTCCAGGCCCTGGATGCCAGGCACTCCCGCAGGTTGCCCGCCT	
QY	1201	GCCCGAGCGTACTGCGAAATGGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAACGGCA	1260
Db	1201		1260
		GCCCGAGCGTACTGCGAAATGGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAACGGCA	
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Db	1261		1320
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		AGCGGGTGTGTGTCGCCGGAGAAAGCCAGGGCTCTGTGTGGGGCCCCCAGAGAGGGA	
QY	1381	CACAGACCCCGCTCGCTGTGACGTGCTCCGCGACACAGACGCCCTGGCAGGTGA	1440
Db	1381		1440
		CACAGACCCCGCTCGCTGTGACGTGCTCCGCGACACAGACGCCCTGGCAGGTGA	
QY	1441	CGGTTTCGTGCGGGCTTGCCTGCGCGGCTGGTGCCCCAGGCTCTGSGGCTCCAGGCA	1500
Db	1441		1500
		CGGTTTCGTGCGGGCTTGCCTGCGCGGCTGGTGCCCCAGGCTCTGSGGCTCCAGGCA	
QY	1501	CAAGAACCGCGCTTCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAAGCATGCCAA	1560
Db	1501		1560
		CAAGAACCGCGCTTCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAAGCATGCCAA	
QY	1561	GCTCTCGCTCAGAGCTGACGTGGAAGATGAGCGTGCGGGACTTGGCTTGGCTGCGCAG	1620
Db	1561		1620
		GCTCTCGCTCAGAGCTGACGTGGAAGATGAGCGTGCGGGACTTGGCTTGGCTGCGCAG	
QY	1621	GAGCCCCAGGGTTGGCTGTGTTCCGGCCCGCAGAGCACCGCTCTCGTGAGGAGATCCTGGC	1680
Db	1621		1680
		GAGCCCCAGGGTTGGCTGTGTTCCGGCCCGCAGAGCACCGCTCTCGTGAGGAGATCCTGGC	
QY	1681	CAAGTTTCTGCACCTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGTCTTCTTTTA	1740
Db	1681		1740
		CAAGTTTCTGCACCTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGTCTTCTTTTA	
QY	1741	TGTCACGAGCACACGTTTCAAAGAACAGGCTCTTTTCTACCGAAAGTCTCTGGAG	1800
Db	1741		1800
		TGTCACGAGCACACGTTTCAAAGAACAGGCTCTTTTCTACCGAAAGTCTCTGGAG	
QY	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGAGGCTGTC	1860

Db	1801	 CAAGTTGCAAAAGCATTTGGAAATACAGACGACTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
Qy	1861	GGAGCAGAGGTCAAGGCAGCATCGGGAAGCAGCCGCGCCCTGCTGACTGATCAGACTCCG	1920
Db	1861	GGAAAGCAGAGGTCAAGGCAGCATCGGGAAGCAGCCGCGCCCTGCTGACTGATCAGACTCCG	1920
Qy	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTAGTCTGCTGGAGC	1980
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTAGTCTGCTGGAGC	1980
Qy	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGCTCTACCTCGAGGGTGAAGGCACGTGT	2040
Db	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGCTCTACCTCGAGGGTGAAGGCACGTGT	2040
Qy	2041	CAGCGTGTCAACTACAGAGGGGGCGGCCGCCCGCGCTCTGCGGGCCCTCTGTGTGGG	2100
Db	2041	CAGCGTGTCAACTACAGAGGGGGCGGCCGCCCGCGCTCTGCGGGCCCTCTGTGTGGG	2100
Qy	2101	CCTGGAGATATCCACAGGGCCTGGCCGCACTTTCGCTGCTGCTGCTGCGGGCCCGAGACC	2160
Db	2101	CCTGGAGATATCCACAGGGCCTGGCCGCACTTTCGCTGCTGCTGCTGCGGGCCCGAGACC	2160
Qy	2161	GCCGCCCTGAGCTGTACTTTTCAAGGTGGATGTGACGGGCGCTAGCACCATCCCCCA	2220
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Db	2221	GGACAGGCTCAGCGAGGTCAATCGGCAGCATCATCAAAACCCAGAACACGTACTGCGTGG	2280
Qy	2281	TCGCTATGCGGTGTCAGAGGCGCCCGCATGAGGACGTCCGCAAGGCCTTCAAGAGCCA	2340
Db	2281	TCGCTATGCGGTGTCAGAGGCGCCCGCATGAGGACGTCCGCAAGGCCTTCAAGAGCCA	2340
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Db	2401	GACAGCCCGGTGAGGGATGCCGTGTCATCGAGCAGAGTCCCTCCCTGAATGAGGCCAG	2460
Qy	2461	CAGTGGCCTCTTCGACGCTCTTCCTAGCGTTCATGTCGCCACCGCGCTGCGCATCAGGG	2520
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Qy	2521	CAAGTCTCTAGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTG	2580
Db	2521	CAAGTCTCTAGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTG	2580
Qy	2581	CAGCCTGTGTCAGGGGACATGAGAACAAAGCTGTTTGGGGGATTCGCGGGAGCGGCT	2640
Db	2581	CAGCCTGTGTCAGGGGACATGAGAACAAAGCTGTTTGGGGGATTCGCGGGAGCGGCT	2640
Qy	2641	GCTCCTGCGTTTGGTGATGATTTCTGTTGTTGTCACCTCACCTCACCCAGCGCAAAAC	2700
Db	2641	GCTCCTGCGTTTGGTGATGATTTCTGTTGTTGTCACCTCACCTCACCCAGCGCAAAAC	2700
Qy	2701	CTTCCTCAGGACCTGTGTCGAGGCTCCCTGAGTATGCTGCGTGGTGAACCTTCGGGA	2760
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Qy	2761	GACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGCACGGCTTTGTTFCAGAT	2820
Db	2761	GACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGCACGGCTTTGTTFCAGAT	2820
Qy	2821	GCGGGCCACGGCCTATTCCTCTGTGCGGCTGCTGCTGGATACCCGGACCCCTGGAGGT	2880
Db	2821	GCGGGCCACGGCCTATTCCTCTGTGCGGCTGCTGCTGGATACCCGGACCCCTGGAGGT	2880
Qy	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCAGCTCTCACTTCAACCG	2940

Db 2881 GCAGACGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGAGTCTCACCTTCAACCG 2940

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Db 2941 CGGCTTCAAGGCTGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG 3000

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QY 3121 TCAGCAAGTTTGGAAAGACCCACATTTTTCCTGCGCGTCATCTCTGACAGCGCCCTCCCT 3180

Db 3121 TCAGCAAGTTTGGAAAGACCCACATTTTTCCTGCGCGTCATCTCTGACAGCGCCCTCCCT 3180

QY 3181 CTGCTACTCCATCTGAAAGCCAAAGAACCCAGGATGTGCTGGGGCCCAAGGGCCCGC 3240

Db 3181 CTGCTACTCCATCTGAAAGCCAAAGAACCCAGGATGTGCTGGGGCCCAAGGGCCCGC 3240

QY 3241 CGGCCCTCTGCTCCAGGCGGTGCAAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Db 3241 CGGCCCTCTGCTCCAGGCGGTGCAAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

QY 3301 GACTCGACACCGTGTACCTAGCTGCCACTCTCTGGGGTCACTCAGGACAGCCAGACGCA 3360

Db 3301 GACTCGACACCGTGTACCTAGCTGCCACTCTCTGGGGTCACTCAGGACAGCCAGACGCA 3360

QY 3361 GCTGAGTGGAGCTCCCGGGAGCAGCGTGTGCTGCTGAGGCGCGCAGCCACCCGCG 3420

Db 3361 GCTGAGTGGAGCTCCCGGGAGCAGCGTGTGCTGCTGAGGCGCGCAGCCACCCGCG 3420

QY 3421 ACTGCCCTCAGACTTCAAGACCATCTGGACTGTATGGCCACCGCCAGCCAGCGCCGA 3480

Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGGACTGTATGGCCACCGCCAGCCAGCGCCGA 3480

QY 3481 GAGCAGACACAGCAGCCCTGTACAGCCGGGCTCTACGTCCCAAGGAGGAGGGCGGCC 3540

Db 3481 GAGCAGACACAGCAGCCCTGTACAGCCGGGCTCTACGTCCCAAGGAGGAGGGCGGCC 3540

QY 3541 CACACCCAGCCGCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTGTGTCGCGCAGGCGCTG 3600

Db 3541 CACACCCAGCCGCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTGTGTCGCGCAGGCGCTG 3600

QY 3601 CATGTCCGGCTGAAGGCTGAGTGTCTCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGGCT 3660

Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCTCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGGCT 3660

QY 3661 GAGTGTCCAGCACACCTGCGCTTTCACCTTCCCCACAGAGGCTGGCGCTCGGCTCCACCCCA 3720

Db 3661 GAGTGTCCAGCACACCTGCGCTTTCACCTTCCCCACAGAGGCTGGCGCTCGGCTCCACCCCA 3720

QY 3721 GGGCCAGCTTTTCCCTCACCAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Db 3721 GGGCCAGCTTTTCCCTCACCAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

QY 3781 CCAGATTGCGCATTTGTTCACCCCTCGCCCTGCGCTCTTTCCTTCCACCCCAACCATCC 3840

Db 3781 CCAGATTGCGCATTTGTTCACCCCTCGCCCTGCGCTCTTTCCTTCCACCCCAACCATCC 3840

QY 3841 AGGTGGAGACCTGTAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900

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QY 3901 CCTGTACACAGCGGAGGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAATGGGGG 3960

Db 3901 CCTGTACACAGCGGAGGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAATGGGGG 3960

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RESULT 9

US-10-105-963-1

; Sequence 1, Application US/10105963

; Publication No. US20030068818A1

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Denning, Chris

; APPLICANT: Clark, A. John

; APPLICANT: Schiuff, J. Michael

; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst

; FILE OF INVENTION: Recombination

; FILE REFERENCE: 731/002

; CURRENT APPLICATION NUMBER: US/10/105,963

; CURRENT FILING DATE: 2002-03-21

; PRIOR APPLICATION NUMBER: US 60/277,811

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 4015

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (56)..(3454)

; OTHER INFORMATION:

US-10-105-963-1

Query Match

Best Local Similarity 100.0%; Score 4015; DB 14; Length 4015;

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 CCGAGTGTGTCAGAGGCTGTGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

QY 361 GCTGTGGAGCGGGCGCGGGGGCGCCCGCCCGAGAGGCTTTCACACAGCGCTGGCGAGCTA 420

Db 361 GCTGTGGAGCGGGCGCGGGGGCGCCCGCCCGAGAGGCTTTCACACAGCGCTGGCGAGCTA 420

QY 421 CCTGCCCAACACAGGTGACGACGCTGGGGGGAGCGGGCGCTGGGGCTGTGCTGGC 480

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Db 541 GGCTCCAGCTGGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGGCGCTGGCCAC 600

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QY 1381 CACAGACCCCGCTCGCTGTGTGAGCTGTCTCCCGACACAGAGCCCTTGGCAGGTGA 1440
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QY 1921 CTTTCATCCCAAGGCTGACGCGGCTGCGCGGATGTGNAACATGACACTACGTCGTGGGAGC 1980
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QY 2341 CGTCTCTACCTTGACAGACCTTCCAGCGGTACATGCGGACGTTCGTGTGCTCACCTGCAAG 2400
Db 2341 CGTCTCTACCTTGACAGACCTTCCAGCGGTACATGCGGACGTTCGTGTGCTCACCTGCAAG 2400
QY 2401 GACCAGCGCGTGAGGATGCGGTCTATCGAGCAGAGCTTCCCTCCCTGAATGAGGCGAG 2460
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;; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;; THERAPEUTIC METHODS
;; NUMBER OF SEQUENCES: 335
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/044,539
;; FILING DATE: 11-Jan-2002
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/912,951
;; FILING DATE: <unknown>
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4015 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 56..3454
;; OTHER INFORMATION: /product="htrt"
;; /note="human telomerase reverse
;; transcriptase (htrt) catalytic protein
;; component"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1

Query Match 100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCGCCGCGGATGCC 60
DB 1 GCAGCGTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCGCCGCGGATGCC 60
QY 61 GCGGCTCCCGCTGCGGAGCCGCTGGCTCCCTGCTGGCAGCCACTACCGCGAGTGCT 120
DB 61 GCGGCTCCCGCTGCGGAGCCGCTGGCTCCCTGCTGGCAGCCACTACCGCGAGTGCT 120
QY 121 GCGGCTGGCCACGTTGCTGGGCGCTGGGGCCCGCCAGGGCTGGGGCTGGTGCAGCGGG 180
DB 121 GCGGCTGGCCACGTTGCTGGGCGCTGGGGCCCGCCAGGGCTGGGGCTGGTGCAGCGGG 180
QY 181 GGACCCGCGGCTTTCGCGCGGCTGGTGGCCCACTGGCTGGTGGCTGGCCCTGGGAGCG 240

DB 181 GGACCCGCGGCTTTCGCGCGGCTGGTGGCCCACTGGCTGGTGGCTGGCTGGGAGCG 240
QY 241 AGGCGCGCGCGCGCGCGCGCGCTCTTCCCGCAGGTGTCTTCCGCTGAAGAGCTGGTGGC 300
DB 241 AGGCGCGCGCGCGCGCGCGCGCTCTTCCCGCAGGTGTCTTCCGCTGAAGAGCTGGTGGC 300
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DB 301 CCGAGTGTCTGAGAGCTGTGCGAGCGCGGCGCGAAGACGTGTGCGCTTGGCTTGGC 360
QY 361 GCTGCTGGAGGGCGCGCGGCGCGCGCGCGCTTCCACACCGAGCTTCCACACCGAGCTT 420
DB 361 GCTGCTGGAGGGCGCGCGGCGCGCGCGCGCTTCCACACCGAGCTTCCACACCGAGCTT 420
QY 421 CCTGCCCAACACCGTGTACCGACCTGCGGGGAGCGGGCGCTGGGGCTGTCTGCTGGC 480
DB 421 CCTGCCCAACACCGTGTACCGACCTGCGGGGAGCGGGCGCTGGGGCTGTCTGCTGGC 480
QY 481 CCGGCTGGGCGACGACGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CCGGCTGGGCGACGACGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GGTCTCCAGCTGCGCTTACCAGGTGTGCGGGCGCGCTGTACCAGCTGCGCGCTGCGCAC 600
DB 541 GGTCTCCAGCTGCGCTTACCAGGTGTGCGGGCGCGCTGTACCAGCTGCGCGCTGCGCAC 600
QY 601 TCAGGCGCGCGCGCGCGCGCGCTAGTGGACCCCGGAGGCGTCTGGATCGCAACGGCG 660
DB 601 TCAGGCGCGCGCGCGCGCGCGCTAGTGGACCCCGGAGGCGTCTGGATCGCAACGGCG 660
QY 661 CTGAACCATAGCTCAGGAGCGCGGGTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGAG 720
DB 661 CTGAACCATAGCTCAGGAGCGCGGGTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGAG 720
QY 721 GAGCGCGGGGCGAGTGCAGCGGAAGTGTCCCTTCCCAAGAGGCGCCAGGCGTGGCGC 780
DB 721 GAGCGCGGGGCGAGTGCAGCGGAAGTGTCCCTTCCCAAGAGGCGCCAGGCGTGGCGC 780
QY 781 TGCCCTTGAGCGGAGCGCGCGCTTGGGAGGGGTCTTGGGCGCCACCGCGGCGAGAC 840
DB 781 TGCCCTTGAGCGGAGCGCGCGCTTGGGAGGGGTCTTGGGCGCCACCGCGGCGAGAC 840
QY 841 GCGTGGACCGAGTACCGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 GCGTGGACCGAGTACCGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CACCTCTTTGGAGGTGCGCTCTCTGGCAGCGCGCACTCCACCCATCCGCTGGGCGCGCA 960
DB 901 CACCTCTTTGGAGGTGCGCTCTCTGGCAGCGCGCACTCCACCCATCCGCTGGGCGCGCA 960
QY 961 GCACACGCGGGCG 1020
DB 961 GCACACGCGGGCG 1020
QY 1021 CCGGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAGGAGAGCTGGC 1080
DB 1021 CCGGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAGGAGAGCTGGC 1080
QY 1081 GCCCTCTCTCTACTCAGCTCTCTGAGCGCCAGCTGACTGGCGCTCGGAGGCTCGTGGGA 1140
DB 1081 GCCCTCTCTCTACTCAGCTCTCTGAGCGCCAGCTGACTGGCGCTCGGAGGCTCGTGGGA 1140
QY 1141 GACCATCTTTCTGGGTTCAGGCGCTTGGATCGCAGGCACTCCCGCAGGTTGCCCGCGCT 1200
DB 1141 GACCATCTTTCTGGGTTCAGGCGCTTGGATCGCAGGCACTCCCGCAGGTTGCCCGCGCT 1200
QY 1201 GCCCGAGGCTACTGGCAATGCGGCGCGCTTTCTTGAGGTGCTTGGGAACACGAGCGCA 1260
DB 1201 GCCCGAGGCTACTGGCAATGCGGCGCGCTTTCTTGAGGTGCTTGGGAACACGAGCGCA 1260
QY 1261 GTGCGGCTACGCGGCTGCTCTCAAGAGCACTGCCCGCTGGAGCTGCGGCTCACCCGAGC 1320

Db	1261	GTGCCCTACGGGTGCTCTCTCAAGACGACACTGCCCGCTGCGAGCTGCGGTCAACCCACG	1320
QY	1321	AGCCGGTGTCTGTGCCGGGAGAACCCAGAGGCTCTGTGGGGCCCCCGAGAGGAGGA	1380
Db	1321	AGCCGGTGTCTGTGCCGGGAGAACCCAGAGGCTCTGTGGGGCCCCCGAGAGGAGGA	1380
QY	1381	CACAGACCCCGTCCGCTGGTACAGTGTCTCGCCAGACACAGACGACCCCTGCGAGGTGTA	1440
Db	1381	CACAGACCCCGTCCGCTGGTACAGTGTCTCGCCAGACACAGACGACCCCTGCGAGGTGTA	1440
QY	1441	CGGCTTCGTGCGGGGCTGCTCGCGCGGCTGGTGTGCCCGCCAGAGCCCTGTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCGTGCGGGGCTGCTCGCGCGGCTGGTGTGCCCGCCAGAGCCCTGTGGGGCTCCAGGCA	1500
QY	1501	CAACGAACCCCGCTTCCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1560
Db	1501	CAACGAACCCCGCTTCCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1561	GCTCTCGCTGACAGGAGCTACCTGGAAGATGAGCGTGGGAGCTGCGGCTGCGGCAG	1620
Db	1561	GCTCTCGCTGACAGGAGCTACCTGGAAGATGAGCGTGGGAGCTGCGGCTGCGGCAG	1620
QY	1621	GAGCCAGGGGTGCGTGTTCGCGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC	1680
Db	1621	GAGCCAGGGGTGCGTGTTCGCGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC	1680
QY	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGTGTCGAGCTGCTCAGGTCTTTCTTTA	1740
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGTGTCGAGCTGCTCAGGTCTTTCTTTA	1740
QY	1741	TGTCAGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTCTGGAG	1800
Db	1741	TGTCAGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTCTGGAG	1800
QY	1801	CAAGTTCGAAAGCATTTGAATCAGACAGACACTTGAAGAGGGTGACGTGCGGAGGTGTC	1860
Db	1801	CAAGTTCGAAAGCATTTGAATCAGACAGACACTTGAAGAGGGTGACGTGCGGAGGTGTC	1860
QY	1861	GGAAGCAGAGTTCAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCG	1920
Db	1861	GGAAGCAGAGTTCAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCG	1920
QY	1921	CTTCACTCCCAAGCTGACGGCTGCGGCCGATGTGAACATGGACTAGTGTGGGAGC	1980
Db	1921	CTTCACTCCCAAGCTGACGGCTGCGGCCGATGTGAACATGGACTAGTGTGGGAGC	1980
QY	1981	CAGAACGTTTCCGACAGAAAGAGGGCCGAGGGTCTCACTCGAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTTCCGACAGAAAGAGGGCCGAGGGTCTCACTCGAGGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTGTCACTAGGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2100
Db	2041	CAGCGTGTCACTAGGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2100
QY	2101	CTTGAAGATATCCACAGGGCTTGGCGCACCTTCGTGCTGCGGTGCGGGGGGGGGGGGG	2160
Db	2101	CTTGAAGATATCCACAGGGCTTGGCGCACCTTCGTGCTGCGGTGCGGGGGGGGGGGGG	2160
QY	2161	GCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGGGTACGACACCATCCCCCA	2220
Db	2161	GCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGGGTACGACACCATCCCCCA	2220
QY	2221	GGACAGGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAACACACTACTGCGTGG	2280
Db	2221	GGACAGGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAACACACTACTGCGTGG	2280
QY	2281	TGGGTATCGGTTCAGAGCCGCCCATGCGGACAGTTCGCGAAGGCCCTTCAAGAGCCA	2340
Db	2281	TGGGTATCGGTTCAGAGCCGCCCATGCGGACAGTTCGCGAAGGCCCTTCAAGAGCCA	2340
QY	2341	CGTCTCTACTTGACAGCTTACAGCGGTACATGGACAGTTCGTCGCTCACTGCAGGA	2400
Db	2341	CGTCTCTACTTGACAGCTTACAGCGGTACATGGACAGTTCGTCGCTCACTGCAGGA	2400

QY	2401	GACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG	2460
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG	2460
QY	2461	CAGTGGCCTCTTCGAGAGTCTTCTACGCTTCATGTGCCACCGCGCTGCGATCAGGGG	2520
Db	2461	CAGTGGCCTCTTCGAGAGTCTTCTACGCTTCATGTGCCACCGCGCTGCGATCAGGGG	2520
QY	2521	CAAGTCTACGCTCCAGTGCAGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG	2580
Db	2521	CAAGTCTACGCTCCAGTGCAGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG	2580
QY	2581	CAGCCTGTGCTACGCGGACATGAGAAAGCTGTTTGGGGGATTCGGCGGACCGGCT	2640
Db	2581	CAGCCTGTGCTACGCGGACATGAGAAAGCTGTTTGGGGGATTCGGCGGACCGGCT	2640
QY	2641	GCTCCTGCGCTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC	2700
Db	2641	GCTCCTGCGCTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC	2700
QY	2701	CTTCTCAGAGCCCTGGTCCGAGGTGCTCCTGAGTATGGCTGCGTGGTGAACCTTGGCGAA	2760
Db	2701	CTTCTCAGAGCCCTGGTCCGAGGTGCTCCTGAGTATGGCTGCGTGGTGAACCTTGGCGAA	2760
QY	2761	GACAGTGTGAACCTTCCCTGTAGAGACAGAGGCCCTGGGTGGACACGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGAACCTTCCCTGTAGAGACAGAGGCCCTGGGTGGACACGGCTTTTGTTCAGAT	2820
QY	2821	GCGGCGCCACGGCTATTCCTGCTGGCGGCTGCTGCTGGATACCGGACCCCTGGAGT	2880
Db	2821	GCGGCGCCACGGCTATTCCTGCTGGCGGCTGCTGCTGGATACCGGACCCCTGGAGT	2880
QY	2881	GCAGAGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Db	2881	GCAGAGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGGAGAACATCGTCCGCAAACTTTTGGGGTCTTCGCGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGAACATCGTCCGCAAACTTTTGGGGTCTTCGCGCTGAAGTG	3000
QY	3001	TCACAGCCTTCTTGGATTTTCAGGTGAACAGCCCTCCAGAGCGGTGTGACCAACATCTA	3060
Db	3001	TCACAGCCTTCTTGGATTTTCAGGTGAACAGCCCTCCAGAGCGGTGTGACCAACATCTA	3060
QY	3061	CAAGATCTCTGCTCAGCGCTACAGTTCACGCTGTCAGCATGTGCTGACGCTCCCATTTCA	3120
Db	3061	CAAGATCTCTGCTCAGCGCTACAGTTCACGCTGTCAGCATGTGCTGACGCTCCCATTTCA	3120
QY	3121	TCAGCAAGTTTGGAGAACCCACATTTTCTGCGCGTATCTCTGACACGCGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAGAACCCACATTTTCTGCGCGTATCTCTGACACGCGCTCCCT	3180
QY	3181	CTGCTACTCTCAATCTGAAAGCCAAAGACGAGGATGTGCTGGGGGGCAAGGGCGCGC	3240
Db	3181	CTGCTACTCTCAATCTGAAAGCCAAAGACGAGGATGTGCTGGGGGGCAAGGGCGCGC	3240
QY	3241	CGGCGCTCTGCGCTCCGAGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
Db	3241	CGGCGCTCTGCGCTCCGAGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
QY	3301	GACTCGACACCGGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGCGCA	3360
Db	3301	GACTCGACACCGGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGCGCA	3360
QY	3361	GCTGAGTTCGAAGCTCCCGGGGACGCTGCTGCTGGAGCGCGAGCCCAACCGCGC	3420
Db	3361	GCTGAGTTCGAAGCTCCCGGGGACGCTGCTGCTGGAGCGCGAGCCCAACCGCGC	3420
QY	3421	ACTGCGCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCGCCACAGCCAGCGCA	3480
Db	3421	ACTGCGCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCGCCACAGCCAGCGCA	3480

Qy	3481	GAGCAGACAC	CAGCAGCCCTGT	CACGCCGGGCTCT	TACGTCC	AGGAGAGG	AGGCGCGGCC	3540		
Db	3481	GAGCAGACAC	CAGCAGCCCTGT	CACGCCGGGCTCT	TACGTCC	AGGAGAGG	AGGCGCGGCC	3540		
Qy	3541	CACACCCAGC	CCCGCACCGCT	TGGGAGTCT	CAGGCGCT	GAGT	GAGTGT	TTGCCCGAGGCGCTG	3600	
Db	3541	CACACCCAGC	CCCGCACCGCT	TGGGAGTCT	CAGGCGCT	GAGT	GAGTGT	TTGCCCGAGGCGCTG	3600	
Qy	3601	CATGTCCGGCT	GAAGGCTGAGT	GTCCGGCT	TGAGGCGT	TGCCAGCA	AGGCGCT	3660		
Db	3601	CATGTCCGGCT	GAAGGCTGAGT	GTCCGGCT	TGAGGCGT	TGCCAGCA	AGGCGCT	3660		
Qy	3661	GAGTGTCCAG	CACACACTT	CTTCACTT	CCCCAC	AGGCTG	GGCGCT	CGCGCTCCACCCCA	3720	
Db	3661	GAGTGTCCAG	CACACACTT	CTTCACTT	CCCCAC	AGGCTG	GGCGCT	CGCGCTCCACCCCA	3720	
Qy	3721	GGGCCAGCT	TTTTCTT	CACAGGAC	CGCGGTT	CCACT	CCCCAC	ATAGGAATAGTCCATCC	3780	
Db	3721	GGGCCAGCT	TTTTCTT	CACAGGAC	CGCGGTT	CCACT	CCCCAC	ATAGGAATAGTCCATCC	3780	
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Db	3781	CCAGATTCGGC	CAATGTTC	ACCCCTCG	CCCTTGCCTT	GCCTT	CCACCC	CCACCATTC	3840	
Qy	3841	AGTGTGAGAC	CCCTG	GAGAAG	CACCTCG	GGGAGCT	CTGGGAA	TTTGGAGT	GACCAAGGTTG	3900
Db	3841	AGTGTGAGAC	CCCTG	GAGAAG	CACCTCG	GGGAGCT	CTGGGAA	TTTGGAGT	GACCAAGGTTG	3900
Qy	3901	CCCTGTATAC	AGGAGG	ACCCCTG	CGATGG	GGGGTCC	CTGTGG	GGTCAAA	TATGGGG	3960
Db	3901	CCCTGTATAC	AGGAGG	ACCCCTG	CGATGG	GGGGTCC	CTGTGG	GGTCAAA	TATGGGG	3960
Qy	3961	GAGGTGCT	GTGGAGT	AAAACT	ACTGA	TATAT	CAGT	TTTTT	CAGTTTTG	4015
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RESULT 12

US-09-432-676-173
; Sequence 173, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
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; TITLE OF INVENTION: NO. US20020164786A1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
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 INFORMATION FOR SEQ ID NO: 173:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4029 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: LOCATION: 1..4029
 OTHER INFORMATION: /note= "preliminary sequence for
 human TR1 cDNA insert of
 plasmid pGRI121"
 SEQUENCE DESCRIPTION: SEQ ID NO: 173:
 US-09-843-676-173

Query Match									
Best Local Similarity 95.9%; Score 3849.2; DB 10; Length 4029;									
Matches 3955; Conservative 0; Mismatches 53; Indels 9; Gaps 8;									
Qy	1	GCAGCGCTGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCGCCACCCGATGCC	60						
Db	1	GCAGCGCTGCTCTGCTGGCAGCTGGGAAGCCCTGGCCCGCCACCCGATGCC	60						
Qy	61	GCAGCGTCCCGCTGCGAGCCGTGGCTCCCTGCTGGCAGCCATACCGGAGTGT	120						
Db	61	GCAGCGTCCCGCTGCGAGCCGTGGCTCCCTGCTGGCAGCCATACCGGAGTGT	120						
Qy	121	GCCGCTGGCCACATTTGTTGGCGGCCCTGGGGCCCCAGGGCTGGCGCTGGTGGCAGCGCG	180						
Db	121	GCCGCTGGCCACATTTGTTGGCGGCCCTGGGGCCCCAGGGCTGGCGCTGGTGGCAGCGCG	180						
Qy	181	GGACCGCGCGGCTTTCCGCGCGCTGGTGGGCCAGTGCCTGGTGTGGTGCCTTGGACGC	240						
Db	181	GGACCGCGCGGCTTTCCGCGCGTGGTGGGCCANTGCTGGTGGCTGGCGGANGN	240						
Qy	241	ACGGCGCGCCCGCGCGCCCTCCCTCCGCGCAGGTGCTGCTGAAGAGTGGTGGC	300						
Db	241	ANGCGNCCCCCGCGCCCTCCCTTCGCGCAGGTGCTGCTGAAGANGTGGTGGC	300						
Qy	301	CCGAGTGTCTGACAGAGCTGTGCGAGGCGCGCGAAGACGTGCTGCGCTTGGCTTCGC	360						
Db	301	CCGAGTGTCTGANAGCTGTGCGANGCGCGCGAANAAGTGTGCGCTTGGCTTCGC	360						
Qy	361	GCTGCTGGACGGGGCGGGGGGGCCCCCGAGGCGCTTACACACAGGCTGGCGACGTA	420						
Db	361	GCTGCTGGACGGGGCGGGGGGGCCCCCGAGGCGCTTACACACAGGCTGGCGACGTA	420						
Qy	421	CTTGCCCAACACAGGTGACCGACGCTGCGGGGGAGCGGGGCGTGGGGCTGCTGTGGG	480						
Db	421	CTTGCCCAACACAGGTGACCGACGCTGCGGGGAGCGGGGCGTGGGGCTGCTGTGGG	480						
Qy	481	CCGCGTGGGGACGAGTGTGTTTCACTGCTGGCACCGCTGGCGCTCTTGTGTGTGT	540						
Db	481	CCGCGTGGGGACGAGTGTGTTTCACTGCTGGCACCGCTGGCGCTCTTGTGTGTGT	540						
Qy	541	GGCTCCCAAGTGGCCCTACCAAGTGTGGGGCGCGCTGTACCACTCGCGGCTGCCAC	600						
Db	541	GGNTCCCAAGTGGCCCTACCAAGTGTGGGGCGCGCTGTACCACTCGCGGCTGCCAC	600						
Qy	601	TCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGCGCTGTGGATGCGAAGCGG	660						
Db	601	TCAGGCCCGGCCCGCCACAGCTANTGGA-CCCGAANGCGTCTGGAT-CCACAGCGG	658						

QY	661	CTGGAACCATAGCGTCAGGAGCGCGGGTCCCCCTGGGCTCCACAGCCCCGGGTGGAG	720	1739	TATGTACGGAGACCACGCTTCAAAGAACAGAGCTCTTTTCTACCGGAAGAGTGTCTGG	1798
Db	659	CTGGAACCATAGCGTCAGGAGCGCGGGTCCCCCTGGG-CTGCCAGCCCCGGGTGGAG	717	1734	TATGTACGGAGACCAGCTTCAAAGAACAGAGCTCTTTTCTACCGGAAGAGTGTCTGG	1793
QY	721	GAGGCGGGGGCAGTGCACGCGAAGTCTGCCGTTGCCCAAGAGGCCAGGGGTGGCGC	780	1799	AGCAAGTTGCAAGCATTTGAATCAGACAGACTTGAAGAGGGTGCAGCTGCCGGAGCTG	1858
Db	718	GAGGCGGGGGCAGTGCACGCGAAGTCTGCCGTTGCCCAAGAGGCCAGGGGTGGCGC	777	1794	AGCAAGTTGCAAGCATTTGAATCAGACAGACTTGAAGAGGGTGCAGCTGCCGGAGCTG	1853
QY	781	TGCCCCGTAGCGGAGCGGACGCCCTTGGGCAAGGGTCTTGCGGCCACCCCGGGCAGGAC	840	1859	TCGGAAGCAGAGGTACAGGAGCATCGGGAAGCCAGGCCGCCCTGTGTAGCTGCAGACTC	1918
Db	778	TGCCCCGTAGCGGAGCGGACGCCCTTGGGCAAGGGTCTTGCGGCCACCCCGGGCAGGAC	837	1854	TCGGAAGCAGAGGTACAGGAGCATCGGGAAGCCAGGCCGCCCTGTGTAGCTGCAGACTC	1913
QY	841	GGGTGACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACGCCGCCGAAAGC	900	1919	CGCTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGAATACGTCGTGGGA	1978
Db	838	GCGTGACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACGCCGCCGAAAGC	897	1914	CGCTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGAATACGTCGTGGGA	1973
QY	901	CACCTCTTTGGAGGGTGCCTCTCTGGCACGGCCACTCCACCCATCCGTGGGCCGCCA	960	1979	GCCAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTG	2038
Db	898	CACCTCTTTGGAGGGTGCCTCTCTGGCACGGCCACTCCACCCATCCGTGGGCCGCCA	957	1974	GCCAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTG	2033
QY	961	GCACACGGGGGGCCCCCATCCACATCGCGGGCCACACGTCTCTGGGACACGCTTGTTC	1020	2039	TTCAGCGTGTCAACTACGAGCGGGCGCGGCCGCCCTCTGTGGCGCTCTGTGTCTG	2098
Db	958	GCACACGGGGGGCCCCCATCCACATCGCGGGCCACCACTG-CTTGGGACACGCTTGTTC	1016	2034	TTTACGCGTGTCAACTACGAGCGGGCGCGGCCGCCCTCTGTGGCGCTCTGTGTCTG	2093
QY	1021	CCCGGTGTAGCGGAGACCAAGCACTTCTCTACTCTCTCCTCAGGGCAAGAGGAGCTGG	1080	2099	GGCTTGACGATATCCACAGGGCCTGGCGCACCTTGTGTGTGTGTGTGTGTGTGTGTGT	2158
Db	1017	CCCGGTGTAGCGGAGACCAAGCACTTCTCTACTCTCTCCTCAGGGCAAGAGGAGCTGG	1074	2094	GGCTTGACGATATCCACAGGGCCTGGCGCACCTTGTGTGTGTGTGTGTGTGTGTGTGT	2153
QY	1081	GGCTCTCTTCTACTC-AGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCGTGG	1139	2159	CCGCCCTGTAGCTGTACTTTGTCAAAGTGTGATGTGACGGGCGCTACGACACCATCCCC	2218
Db	1075	NCCCTCTCTTCTACTCAATATATCTGAGGCCAGCTGACTGGCTTCGGGAGTTCGTG	1134	2154	CCGCCCTGTAGCTGTACTTTGTCAAAGTGTGATGTGACGGGCGCTACGACACCATCCCC	2213
QY	1140	AGACATCTTTCGGGTTCAGGCCCTGTGATGCCAGGGACTCCCCGACAGTTGCCCGCC	1199	2219	CAGGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAACCCAGAACACGTACTGGTG	2278
Db	1135	GAGACATCTTTCGGGTTCAGGCCCTGTGATGCCA-GGATTCCTCCGACAGTTGCCCGCC	1193	2214	CAGGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAACCCAGAACACGTACTGGTG	2273
QY	1200	TGCCCCAGCGCTACTGGCAATCGCGCCCTGTCTTCTGGAGTGTCTTGGAAACAGCGC	1259	2279	CGTGGTGTATGCCGTGTCCAGAGGCGGCCCATGGGCACGTCCGCAAGGCTTCAAGAGC	2338
Db	1194	TGCCCCAGCGCTACTGGCAATCGCGCCCTGTCTTCTGGAGTGTCTTGGAAACAGCGC	1253	2274	CGTGGTGTATGCCGTGTCCAGAGGCGGCCCATGGGCACGTCCGCAAGGCTTCAAGAGC	2333
QY	1260	AGTGCCCTTACGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGGGGTCAACCCAG	1319	2339	CAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGAGTTCGTGGCTCACCTGCAG	2398
Db	1254	AGTGCCCTTACGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGGGGTCAACCCAG	1313	2334	CAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGAGTTCGTGGCTCACCTGCAG	2393
QY	1320	CAGCCGGTGTCTGCGGGAGAACGCCAGGGCTGTGTGGGGCCCCCGAGGAGGAGG	1379	2399	GAGACAGCCCGCTGAGGGATGCGTGTATCGAGCAGAGTCTCTCCCTGAATGAGGCC	2458
Db	1314	CAGCCGGTGTCTGCGGGAGAACGCCAGGGCTGTGTGGGGCCCCCGAGGAGGAGG	1373	2394	GAACAAGCCCGCTGAGGGATGCGTGTATCGAGCAGAGTCTCTCCCTGAATGAGGCC	2453
QY	1380	-ACACAGACCCCGTCCGCTGGTGCAGCTGCTCCGCCAGCACAGACGCCCTGGCAGGTG	1438	2459	AGCAGTGGCCCTCTTCGACGCTCTTCTACGCTTATGTGCCACACAGCCGTGCCCATCAGG	2518
Db	1374	ACACAGACCCCGTCCGCTGGTGCAGCTGCTCCGCCAGCACAGACGCCCTGGCAGGTG	1433	2454	AGCAGTGGCCCTCTTCGACGCTCTTCTACGCTTATGTGCCACACAGCCGTGCCCATCAGG	2513
QY	1439	TAGGGCTGTGTGGGGCTGCTTGCCTGGGCTGGTCCCGCCAGGCGCTCTGGGGCTCCAGG	1498	2519	GGCAAGTCTTACCTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTC	2578
Db	1434	TAGGGCTGTGTGGGGCTGCTTGCCTGGGCTGGTCCCGCCAGGCGCTCTGGGGCTCCAGG	1493	2514	GGCAAGTCTTACCTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTC	2573
QY	1499	CACAAGAACCGCGCTCTCTCAGGAACACCAAGAGTTATCTCTCTGGGGAAGCATGCC	1558	2579	TGCAGCGTGTGTCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGG	2638
Db	1494	CACAAGAACCGCGCTCTCTCAGGAACACCAAGAGTTATCTCTCTGGGGAAGCATGCC	1553	2574	TGCAGCGTGTGTCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGG	2633
QY	1559	AGCTCTCGCTCAGGAGCTGAGTGAAGATGAGGTGCGGGACGTGGCGTGGCTGGCGCGC	1618	2639	CTGCTCTCGGTTTGGTGGATGATTTCTTCTGTGTGACACTCACCTCACCCACGCGAAA	2698
Db	1554	AGCTCTCGCTCAGGAGCTGAGTGAAGATGAGGTGCGGGACGTGGCGTGGCTGGCGCGC	1613	2634	CTGCTCTCGGTTTGGTGGATGATTTCTTCTGTGTGACACTCACCTCACCCACGCGAAA	2693
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				2819	ATGCCGGCCACCGGCTATTCCCTGTGTGGGCTGTGTGGATACCCCGGACCCCTGGAG	2878

CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/053,758
 FILING DATE: 18-Jan-2002
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 173:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4029 base pairs
 TYPE: nucleic acid
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 MOLECULE TYPE: cDNA
 FEATURE:
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QY	181	GGACCCGCGGCTTCCGCGCGCTGCTGGCCCGAGTGCCTGGTGGTGGCTGGGAGCG	240
DB	181	GGACCCGCGGCTTCCGCGCGCTGCTGGCCCGAGTGCCTGGTGGTGGCTGGGAGCG	240
QY	241	ACGGCGCGCGCGCGCGCGCTTCCCTGCGCAGAGTGTCTGCGCAGAGAGAGTGTGCG	300
DB	241	ANGCGCGCGCGCGCGCGCTTCCCTTCCGCGAGGTGTCTGCGCAGAGTGTGCGTGC	300
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QY	361	GCTGCTGGAGCGGGGCGCGCGGGGCCCCCGGAGGCTTTCACACAGAGCTGCGCAGCTA	420
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DB	421	CCTGCCCAACACGGGTGACGAGCACTGTGGGGGAGCGGGGCTGGGGGCTGCTGTGCG	480
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DB	481	CCGCGTGGGCGACGAGCTGCTGTTTACCTGTGCGACGCTGCGCGCTCTTTTGTGTGGT	540
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DB	1314	CAGCGGCTGTGTGCGCGGAGAACGCCAGGGCTCTGTGTGGGCGCCCGCAGGAGGAGG	1373
QY	1380	-ACACAGACCCCGCTGCTGGTGTGAGCTGCTCCCGCAGCAGCAGACGAGCCCTTGGCAG	1438
DB	1374	ACACAGACCCCGCTGCTGGTGTGAGCTGCTCCCGCAGCAGCAGACGAGCCCTTGGCAG	1433

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Db	3654	CTGAGTGTCCAGCACACCTGCCGCTTCACTTCCCCACAGGCTGGCGCTCGGTCACACC	3713
Qy	3719	CAGGGCCAGCTTTTCCCTACAGAGGCCGGCTTCCACTCCACACATAGGAATAGTCCAT	3778
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; Sequence 173, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030044953A1 Telomerase

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ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/10/054,295
 FILING DATE: 18-Jan-2002
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/854,050
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple Randolph T.
 REGISTRATION NUMBER: 56,429
 REFERENCE/DOCKET NUMBER: 015389-00293005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200

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TELEFAX: (415) 576-0300
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SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
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plasmid pGRN121"
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US-10-054-295-173

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